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HUMAN MEMBRANE CHANNEL PROTEINS

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of human membrane
5 channel proteins and to the use of these sequences in the diagnosis, treatment, and prevention of
cell proliferative, immune/inflammatory, transport/secretory, osmoregulatory, muscular,
cardiovascular, and neurological disorders.

BACKGROUND OF THE INVENTION

10 Channel proteins facilitate the transport of hydrophilic molecules across membranes by
forming aqueous pores that can perforate a lipid bilayer. Many channels consist of protein
complexes formed by the assembly of multiple subunits, at least one of which is an integral
membrane protein that contributes to formation of the pore. In some cases, the pore is constructed
to selectively allow passage of only one or a few molecular species. Distinct types of membrane
15 channels that differ greatly in their distribution and selectivity include: (1) aquaporins, which
transport water; (2) protein-conducting channels, which transport proteins across the endoplasmic
reticulum membrane; (3) gap junctions, which facilitate diffusion of ions and small organic
molecules between neighboring cells; and (4) ion channels, which regulate ion flux through
various membranes.

20 Aquaporins

Aquaporins (AQP) are channels that transport water and, in some cases, nonionic small
solutes such as urea and glycerol. Water movement is important for a number of physiological
processes including renal fluid filtration, aqueous humor generation in the eye, cerebrospinal fluid
production in the brain, and appropriate hydration of the lung. A variety of aquaporins have been
25 found in higher animals, plants and microorganisms. The mammalian aquaporins appear to have
selective expression in particular tissues, with AQP0 localized to lens epithelium; AQP1 localized
to many tissues including red blood cells, kidney, eye, lung, choroid plexus, bile duct, and
vascular epithelium; AQP2 localized to the apical membrane of kidney collecting duct cells; AQP3
localized to kidney, colon, trachea, urinary bladder, skin, and sclera of eye; AQP4 localized to
30 kidney, colon, trachea, stomach, skeletal muscle, spinal cord, brain, and retina; AQP5 localized to
the apical membranes of exocrine tissues; AQP6 localized to kidney; and AQP7 localized to testis
(King, L.S. and P. Agre (1996) *Annu. Rev. Physiol.* 58:619-648; Ishibashi, K. et al. (1997) *J. Biol.*
Chem. 272:20782-20786). AQP9 is expressed in peripheral leukocytes, less abundantly in liver,
even less in lung and spleen, and not at all in thymus tissue (Ishibashi, K. et al. (1998) *Biochem.*

Biophys. Res. Commun. 244:268-274).

Aquaporins are members of the major intrinsic protein (MIP) family of membrane transporters. MIP family proteins are composed of four subunits, each of which may span the membrane six times, and have their N-and C-termini facing the cell cytoplasm. Proteins from
5 bacteria, yeast, plants, and animals have been shown to be members of the MIP family (Reizer, J. et al. (1993) Crit. Rev. Biochem. 28:235-257). Aquaporin subunits are integral membrane proteins with six transmembrane regions and two conserved Asn-Pro-Ala (NPA) boxes (which are sometimes found as Asn-Pro-Ser) found in loop regions between the transmembrane regions (King, supra; Ishibashi, (1997) supra). The study of aquaporins may have relevance to
10 understanding edema formation and fluid balance in both normal physiological and disease states (King, supra). Mutations in AQP2 cause autosomal recessive nephrogenic diabetes insipidus (Online Mendelian Inheritance in Man (OMIM) *107777 Aquaporin 2; AQP2). Reduced AQP4 expression in skeletal muscle may be associated with Duchenne muscular dystrophy (Frigeri, A. et al. (1998) J. Clin. Invest. 102:695-703). Mutations in AQP0 cause autosomal dominant cataracts
15 in mice (OMIM *154050 Major Intrinsic Protein of Lens Fiber; MIP).

Protein-Conducting Channels

Secreted and integral membrane proteins are transported from the cytoplasm to the endoplasmic reticulum (ER) through protein-conducting channels in the ER membrane. The channel is used for both co- and post-translational translocation. In the co-translational process,
20 transport is initiated by the action of a cytoplasmic signal recognition particle (SRP) which recognizes a signal sequence on a growing, nascent polypeptide and binds the polypeptide and its ribosome complex to the ER membrane through an SRP receptor located on the membrane. The ribosome complex, together with the attached polypeptide, becomes membrane bound. As the nascent chain emerges from the ribosome, it is fed into the channel and across the ER membrane.
25 The post-translational process also requires a signal sequence on the protein to be translocated, but does not require an SRP. The protein enters the channel and is driven across the ER membrane by the hydrolysis of adenosine triphosphate (ATP) by BiP, an ATPase and molecular chaperone in the ER lumen.

The protein-conducting channel, termed the Sec61p complex, is composed of multiple,
30 probably two, heterotrimers of three membrane proteins, the alpha, beta, and gamma subunits of Sec61p. The Sec61p complex forms a ring structure visible by electron microscopy (EM). EM and quenching experiments indicate a channel diameter of 20 to 60 Å. Association of the Sec61p complex with the ribosome and with the proteins Sec62p, Sec63p, Sec71p, Sec72p, BiP, and TRAM (translocating chain-associating membrane protein) is required for some of the channel's

functions. The Sec61p alpha subunit contains ten membrane-spanning segments and has been found to line the path of the translocating polypeptide chain from one side of the membrane to the other. The sequences of dog and rat Sec61p alpha genes have been determined. Homologs of the mammalian Sec61p alpha are found in the yeast Saccharomyces cerevisiae (Sec61p) and in
5 bacteria (SecYp). (See Görlich, D. et al. (1992) Cell 71:489-503; Matlack, K.E.S. et al. (1998) Cell 92:381-390.)

Defects in protein trafficking to organelles or to the cell surface are involved in numerous human diseases and disorders including cystic fibrosis, glucose-galactose malabsorption syndrome, hypercholesterolemia, diabetes mellitus, diabetes insipidus, hyper- and hypoglycemia,
10 Grave's disease, goiter, Cushing's disease, and Addison's disease. Cancer cells secrete excessive amounts of hormones or other biologically active peptides.

Gap Junctions

Gap junctions (also called connexons) are channels that function chemically and electrically to couple the cytoplasm of neighboring cells in many tissues. Gap junctions function
15 as electrical synapses for intercellular propagation of action potentials in excitable tissues. In nonexcitable tissues, gap junctions have roles in tissue homeostasis, coordinated physiological response, metabolic cooperation, growth control, and the regulation of development and differentiation. Gap junctions help to synchronize heart and smooth muscle contraction, speed
neural transmission, and propagate extracellular signals. Gap junctions can open and close in
20 response to particular stimuli (e.g., pH, Ca^{+2} , and cAMP). The effective pore size of a gap junction is approximately 1.5 nm, which enables small molecules (e.g., those under 1000 daltons) to diffuse freely through the pore. Transported molecules include ions, small metabolites, and second messengers (e.g., Ca^{+2} and cAMP).

Each connexon is composed of six identical subunits called connexins. At least thirteen
25 distinct connexin proteins exist, with each having similar structures but differing tissue distributions. Structurally, the connexins are integral membrane proteins with four putative membrane spanning regions and N- and C-termini oriented towards the cell cytoplasm. Conserved regions include the membrane spanning regions and two extracellular loops. The variable regions, which are two cytoplasmic loops and the C-terminal region, may be responsible for the regulation
30 of different connexins. (See Hennemann, H. et al. (1992) J. Biol. Chem. 267:17225-17233; PRINTS PR00206 connexin signature.)

Connexins have many disease associations. Female mice lacking connexin 37 (Cx37) are infertile due to the absence of the oocyte-granulosa cell signaling pathway. Mice lacking Cx43 die shortly after birth and show cardiac defects reminiscent of some forms of stenosis of the

pulmonary artery in humans. Mutations in Cx32 are associated with the X-linked form of Charcot-Marie-Tooth disease, a motor and sensory neuropathy of the peripheral nervous system. Cx26 is expressed in the placenta, and Cx26-deficient mice show decreased transplacental transport of a glucose analog from the maternal to the fetal circulation. In humans, Cx26 has been identified as the first susceptibility gene for non-syndromic sensorineural autosomal deafness. Cx46 is expressed in lens fiber cells, and Cx46-deficient mice develop early-onset cataracts that resemble human nuclear cataracts. (See Nicholson, S.M. and R. Bruzzone (1997) Curr. Biol. 7:R340-R344.)

Ion Channels

The electrical potential of a cell is generated and maintained by controlling the movement of ions across the plasma membrane. The movement of ions requires ion channels, which form an ion-selective pore within the membrane. There are two basic types of ion channel: ion transporters and gated ion channels. Ion transporters utilize the energy obtained from ATP hydrolysis to actively transport an ion against the ion's concentration gradient. Gated ion channels allow passive flow of an ion down the ion's electrochemical gradient under restricted conditions. Together, these types of ion channels generate, maintain, and utilize an electrochemical gradient that is used in 1) electrical impulse conduction down the axon of a nerve cell, 2) transport of molecules into cells against concentration gradients, 3) initiation of muscle contraction, and 4) endocrine cell secretion.

Ion channels share common structural and mechanistic themes. The channel consists of four or five subunits or protein monomers that are arranged like a barrel in the plasma membrane. Each subunit typically consists of six potential transmembrane segments (S1, S2, S3, S4, S5, and S6). The center of the barrel forms a pore lined by α -helices or β -strands. The side chains of the amino acid residues comprising the α -helices or β -strands establish the charge (cation or anion) selectivity of the channel. The degree of selectivity, or what specific ions are allowed to pass through the channel, depends on the diameter of the narrowest part of the pore.

Ion Transporters

Ion transporters generate and maintain the resting electrical potential of a cell. Utilizing the energy derived from ATP hydrolysis, they transport ions against the ion's concentration gradient. These transmembrane ATPases are divided into three families. The vacuolar (V) class of ion transporters includes H^+ pumps on intracellular organelles, such as lysosomes and Golgi. V-class ion transporters are responsible for generating the low pH within the lumen of these organelles that is required for function. The coupling factor (F) class consists of H^+ pumps in the mitochondria. F-class ion transporters utilize a proton gradient to generate ATP from ADP and

inorganic phosphate (P_i). The phosphorylated (P) class ion transporters, including Na^+ - K^+ ATPase, Ca^{+2} -ATPase, and H^+ -ATPase, are activated by a phosphorylation event. P-class ion transporters are responsible for maintaining resting potential distributions such that cytosolic concentrations of Na^+ and Ca^{+2} are low and cytosolic concentration of K^+ is high. The resting potential of the cell is utilized in many processes involving carrier proteins and gated ion channels. Carrier proteins utilize the resting potential to transport molecules into and out of the cell. Amino acid and glucose transport into many cells is linked to sodium ion co-transport (symport) so that the movement of Na^+ down an electrochemical gradient drives transport of the other molecule up a concentration gradient. Similarly, cardiac muscle links transfer of Ca^{+2} out of the cell with transport of Na^+ into the cell (antiport).

Gated Ion Channels

Gated ion channels control ion flow by regulating the opening and closing of pores. The ability to control ion flux through various gating mechanisms allows ion channels to mediate such diverse signaling and homeostatic functions as neuronal and endocrine signaling, muscle contraction, fertilization, and regulation of ion and pH balance. Gated ion channels are categorized according to the manner of regulating the gating function. Mechanically-gated channels open their pores in response to mechanical stress; voltage-gated channels (e.g., Na^+ , K^+ , Ca^{+2} , and Cl^- channels) open their pores in response to changes in membrane potential; and ligand-gated channels (e.g., acetylcholine-, serotonin-, and glutamate- gated cation channels, and GABA- and glycine- gated chloride channels) open their pores in the presence of a specific ion, nucleotide, or neurotransmitter. The gating properties of a particular ion channel (i.e., its threshold for and duration of opening and closing) are sometimes modulated by association with auxiliary channel proteins and/or post translational modifications, such as phosphorylation. The pore forming subunits of voltage-gated and transmitter-gated cation channels form two distinct superfamilies of conserved multipass membrane proteins.

Voltage-gated Na^+ and K^+ channels are necessary for the function of electrically excitable cells such as nerve, endocrine, and muscle cells. Action potentials, which lead to neurotransmitter release and muscle contraction, arise from large, transient changes in the permeability of the membrane to Na^+ and K^+ ions. Depolarization of the membrane beyond the threshold level opens voltage-gated Na^+ channels. Sodium ions flow into the cell, further depolarizing the membrane and opening more voltage-gated Na^+ channels, thus propagating the depolarization down the length of the cell. Depolarization also opens voltage-gated K^+ channels. Consequently, potassium ions flow outward, leading to repolarization of the membrane. Voltage-gated channels utilize charged residues in the fourth transmembrane segment (S4) to sense voltage change. The open

state lasts only about 1 millisecond, at which time the channel spontaneously converts into an inactive state that cannot be opened irrespective of the membrane potential. Inactivation is mediated by the channel's N-terminus, which acts as a plug that closes the pore. The transition from an inactive to a closed state requires a return to resting potential.

5 Na⁺ channels isolated from rat brain tissue are heterotrimeric complexes composed of a 260 kDa pore-forming α subunit that associates with two smaller auxiliary subunits, β 1 and β 2. The β 2 subunit is an integral membrane glycoprotein that contains an extracellular Ig domain, and its association with α and β 1 subunits correlates with increased function of the channel, a change in the channel's gating properties, as well as an increase in whole cell capacitance (Isom, L.L. et
10 al. (1995) Cell 83:433-442).

K⁺ channels are located in all cell types, and may be regulated by voltage, ATP concentration, or second messengers such as Ca⁺⁺ and cAMP. In non-excitabile tissue, K⁺ channels are involved in protein synthesis, control of endocrine secretions, and the maintenance of osmotic equilibrium across membranes. In neurons and other excitable cells, in addition to regulating
15 action potentials and repolarizing membranes, K⁺ channels are responsible for setting resting membrane potential. The cytosol contains non-diffusible anions and, to balance this net negative charge, the cell contains a Na⁺-K⁺ pump and ion channels that provide the redistribution of Na⁺, K⁺, and Cl⁻. The pump actively transports Na⁺ out of the cell and K⁺ into the cell in a 3:2 ratio. Ion channels in the plasma membrane allow K⁺ and Cl⁻ to flow by passive diffusion. Because of
20 the high negative charge within the cytosol, Cl⁻ flows out of the cell. The flow of K⁺ is balanced by an electromotive force pulling K⁺ into the cell, and a K⁺ concentration gradient pushing K⁺ out of the cell. Thus, the resting membrane potential is primarily regulated by K⁺ flow (Salkoff, L. and T. Jegla (1995) Neuron 15:489-492).

K⁺ pore-forming subunits generally have six transmembrane-spanning domains with a
25 short region between the fifth and sixth transmembrane regions that senses membrane potential; and the amino and carboxy termini are located intracellularly. In mammalian heart, the duration of ventricular action potential is controlled by a K⁺ current. Thus, the K⁺ channel is central to the control of heart rate and rhythm. K⁺ channel dysfunctions are associated with a number of renal diseases including hypertension, hypokalemia, and the associated Bartter's syndrome and
30 Getelman's syndrome, as well as neurological disorders including epilepsy. K⁺ channels have been implicated in Alzheimer's disease by observations that a significant component of senile plaques, beta amyloid or A beta, also blocks voltage-gated potassium channels in hippocampal neurons. (See Ant s, L.M. et al. (1998) Seminar Nephrol. 18:31-45; Stoffel, M. and L.Y. Jan (1998) Nat. Genet. 18:6-8; Madeja, M. et al. (1997) Eur. J. Neurosci. 9:390-395; Good, T.A. et al.

(1996) Biophys. J. 70:296-304.)

Voltage-gated Ca^{+2} channels are involved in presynaptic neurotransmitter release, and heart and skeletal muscle contraction. The voltage-gated Ca^{+2} channels from skeletal muscle (L-type) and brain (N-type) have been purified and, though their functions differ dramatically, they have similar subunit compositions. The channels are composed of three subunits. The α_1 subunit forms the membrane pore and voltage sensor, while the $\alpha_2\delta$ and β subunits modulate the voltage-dependence, gating properties, and the current amplitude of the channel. These subunits are encoded by at least six α_1 , one $\alpha_2\delta$, and four β genes. A fourth subunit, γ , has been identified in skeletal muscle. (See Walker, D. et al. (1998) J. Biol. Chem. 273:2361-2367; Jay, S.D. et al. (1990) Science 248:490-492.)

Chloride channels are necessary in endocrine secretion and in regulation of cytosolic and organelle pH. In secretory epithelial cells, Cl^- enters the cell across a basolateral membrane through an Na^+ , K^+/Cl^- cotransporter, accumulating in the cell above its electrochemical equilibrium concentration. Secretion of Cl^- from the apical surface, in response to hormonal stimulation, leads to flow of Na^+ and water into the secretory lumen. The cystic fibrosis transmembrane conductance regulator (CFTR) is a chloride channel encoded by the gene for cystic fibrosis, a common fatal genetic disorder in humans. Loss of CFTR function decreases transepithelial water secretion and, as a result, the layers of mucus that coat the respiratory tree, pancreatic ducts, and intestine are dehydrated and difficult to clear. The resulting blockage of these sites leads to pancreatic insufficiency, "meconium ileus," and devastating "chronic obstructive pulmonary disease" (Al-Awqati, Q. et al. (1992) J. Exp. Biol. 172:245-266).

Many intracellular organelles contain H^+ -ATPase pumps that generate transmembrane pH and electrochemical differences by moving protons from the cytosol to the organelle lumen. If the membrane of the organelle is permeable to other ions, then the electrochemical gradient can be abrogated without affecting the pH differential. In fact, removal of the electrochemical barrier allows more H^+ to be pumped across the membrane, increasing the pH differential. Cl^- is the sole counterion of H^+ translocation in a number of organelles, including chromaffin granules, Golgi vesicles, lysosomes, and endosomes. Functions that require a low vacuolar pH include uptake of small molecules such as biogenic amines in chromaffin granules, processing of vacuolar constituents such as pro-hormones by proteolytic enzymes, and protein degradation in lysosomes (Al-Awqati, *supra*).

Ligand-gated channels open their pores when an extracellular or intracellular mediator binds to the channel. Neurotransmitter-gated channels are channels that open when a neurotransmitter binds to their extracellular domain. These channels exist in the postsynaptic

membrane of nerve or muscle cells. There are two types of neurotransmitter-gated channels. Sodium channels open in response to excitatory neurotransmitters, such as acetylcholine, glutamate, and serotonin. This opening causes an influx of Na⁺ and produces the initial localized depolarization that activates the voltage-gated channels and starts the action potential. Chloride
5 channels open in response to inhibitory neurotransmitters, such as γ -aminobutyric acid (GABA) and glycine, leading to hyperpolarization of the membrane and the subsequent generation of an action potential.

Ligand-gated channels can be regulated by intracellular second messengers. Calcium-activated K⁺ channels are gated by internal calcium ions. In nerve cells, an influx of calcium
10 during depolarization opens K⁺ channels to modulate the magnitude of the action potential (Ishi, T.M. et al. (1997) Proc. Natl. Acad. Sci. USA 94:11651-11656). Cyclic nucleotide-gated (CNG) channels are gated by cytosolic cyclic nucleotides. The best examples of these are the cAMP-gated Na⁺ channels involved in olfaction and the cGMP-gated cation channels involved in vision. Both systems involve ligand-activation of a G-protein coupled receptor which then alters the level
15 of cyclic nucleotide within the cell. In olfaction, binding of an odorant to the receptor activates adenylate cyclase, leading to a rise in cytosolic cAMP. The cAMP binds to the cAMP-gated Na⁺ channel causing an influx of Na⁺, depolarization of the membrane, and initiation of a nerve impulse that travels along the axon to the brain. In vision, light activation of rhodopsin leads to activation of cGMP phosphodiesterase, which hydrolyzes cGMP. As a result, cytosolic cGMP
20 levels drop, cGMP dissociates from cGMP-gated cation channels, and the channels close, resulting in hyperpolarization of the membrane. (See Zagotta, W.M. and S.A. Siegelbaum (1996) Annu. Rev. Neurosci. 19:235-263; Molday, R.S. and L.L. Molday (1998) Vision Res. 38:1315-1323.)

The subunits or monomers of an ion channel may be identical or different. CNG channels, for example, consist of α and β subunits that differ from each other at the N-terminal
25 cytoplasmic tail. The central pore formed by the barrel arrangement is lined by an antiparallel β -sheet, the pore (P) region, contained within each subunit. This region also contains information specifying the ion selectivity for the channel. In the case of K⁺ channels, a GYG tripeptide is involved in this selectivity (Ishi et al., supra). In voltage-gated channels, one of the transmembrane domains contains regularly spaced, positively charged amino acids that act as a
30 voltage-sensor. In CNG channels, a region in the C-terminal cytoplasmic domain acts as a cyclic nucleotide binding site (Zagotta and Siegelbaum, supra). Ion channels also have a domain that functions in inactivation of the channel. In CNG K⁺ channels, the inactivation domain is on the N-terminal cytoplasmic tail of the β -subunit. This domain acts as a tethered ball to block ion flow through the pore. This domain is also expressed as a separate protein, a glutamic acid-rich protein

(GARP), by alternative splicing and may act as an independent regulator of pore activity (Sautter, A. et al. (1997) Molec. Brain Res. 48:171-175).

Ion channels are essential to a wide range of physiological functions including neuronal signaling, muscle contraction, cardiac pacemaking, hormone secretion, and cell proliferation. Ion channels are expressed in a number of tissues where they are implicated in a variety of processes. CNG channels, while abundantly expressed in photoreceptor and olfactory sensory cells, are also found in kidney, lung, pineal, retinal ganglion cells, testis, aorta, and brain. Calcium-activated K⁺ channels may be responsible for the vasodilatory effects of bradykinin in the kidney and for shunting excess K⁺ from brain capillary endothelial cells into the blood. They are also implicated in repolarizing granulocytes after agonist-stimulated depolarization (Ishi et al., supra). Ion channels have been the target for many drug therapies. Neurotransmitter-gated channels have been targeted in therapies for treatment of insomnia, anxiety, depression, and schizophrenia. Voltage-gated channels have been targeted in therapies for arrhythmia, ischemic stroke, head trauma, and neurodegenerative disease (Taylor, C.P. and L.S. Narasimhan (1997) Adv. Pharmacol. 39:47-98).

The discovery of new human membrane channel proteins and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of cell proliferative, immune/inflammatory, transport/secretory, osmoregulatory, muscular, cardiovascular, and neurological disorders.

SUMMARY OF THE INVENTION

The invention features substantially purified polypeptides, human membrane channel proteins, referred to collectively as "MECHP" and individually as "MECHP-1," "MECHP-2," "MECHP-3," "MECHP-4," "MECHP-5," "MECHP-6," "MECHP-7," "MECHP-8," "MECHP-9," "MECHP-10," "MECHP-11," "MECHP-12," "MECHP-13," "MECHP-14," "MECHP-15," "MECHP-16," "MECHP-17", and "MECHP-18." In one aspect, the invention provides a substantially purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, and fragments thereof.

The invention further provides a substantially purified variant having at least 95% amino acid sequence identity to at least one of the amino acid sequences selected from the group consisting of SEQ ID NO:1-18 and fragments thereof. The invention also provides an isolated and purified polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18 and fragments thereof. The invention also includes an isolated and purified polynucleotide variant having at least 95% polynucleotide sequence

identity to the polynucleotide encoding the polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO:1-18 and fragments thereof.

5 Additionally, the invention provides an isolated and purified polynucleotide which hybridizes under stringent conditions to the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18 and fragments thereof. The invention also provides an isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide encoding the polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO:1-18 and fragments thereof.

10 The invention also provides a method for detecting a polynucleotide in a sample containing nucleic acids, the method comprising the steps of (a) hybridizing the complement of the polynucleotide sequence to at least one of the polynucleotides of the sample, thereby forming a hybridization complex; and (b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of a polynucleotide in the sample. In one aspect, the method further comprises amplifying the polynucleotide prior to hybridization.

15 The invention also provides an isolated and purified polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:19-36, and fragments thereof. The invention further provides an isolated and purified polynucleotide variant having at least 95% polynucleotide sequence identity to the polynucleotide sequence selected from the group consisting of SEQ ID NO:19-36 and fragments thereof. The invention also provides an isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:19-36 and fragments thereof.

20 The invention further provides an expression vector containing at least a fragment of the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18 and fragments thereof. In another aspect, the expression vector is contained within a host cell.

25 The invention also provides a method for producing a polypeptide, the method comprising the steps of: (a) culturing the host cell containing an expression vector containing at least a fragment of a polynucleotide under conditions suitable for the expression of the polypeptide; and (b) recovering the polypeptide from the host cell culture.

30 The invention also provides a pharmaceutical composition comprising a substantially purified polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:1-18 and fragments thereof, in conjunction with a suitable pharmaceutical carrier.

The invention further includes a purified antibody which binds to a polypeptide selected

from the group consisting of SEQ ID NO:1-18 and fragments thereof. The invention also provides a purified agonist and a purified antagonist to the polypeptide.

The invention also provides a method for treating or preventing a disorder associated with decreased expression or activity of MECHP, the method comprising administering to a subject in
5 need of such treatment an effective amount of a pharmaceutical composition comprising a substantially purified polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:1-18 and fragments thereof, in conjunction with a suitable pharmaceutical carrier.

The invention also provides a method for treating or preventing a disorder associated with
10 increased expression or activity of MECHP, the method comprising administering to a subject in need of such treatment an effective amount of an antagonist of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18 and fragments thereof.

BRIEF DESCRIPTION OF THE FIGURES AND TABLES

15 Figure 1 shows the amino acid sequence alignment between MECHP-1 (1568324; SEQ ID NO:1) and rat glutamic acid-rich protein (GI 2924369; SEQ ID NO:37), produced using the BLAST search tool.

Figure 2 shows the amino acid sequence alignment among MECHP-2 (4094907; SEQ ID NO:2), Drosophila voltage-gated potassium channel (GI 116443; SEQ ID NO:38), and P. penicillatus potassium channel α -subunit (GI 1763619; SEQ ID NO:39), produced using the
20 multisequence alignment program of LASERGENE software (DNASTAR, Madison WI).

Figures 3A and 3B show the amino acid sequence alignment between MECHP-3 (518158; SEQ ID NO:3) and rat calcium-activated potassium channel rSK3 (GI 2564072; SEQ ID NO:40), produced using the multisequence alignment program of LASERGENE software.

25 Figures 4A, 4B, and 4C show the amino acid sequence alignment among MECHP-4 (602926; SEQ ID NO:4), Drosophila voltage-gated potassium channel (GI 116443; SEQ ID NO:38) and P. penicillatus potassium channel α -subunit (GI 1763619; SEQ ID NO:39), produced using the multisequence alignment program of LASERGENE software.

Figures 5A and 5B show the amino acid sequence alignment between MECHP-5 (922119; SEQ ID NO:5) and rat aquaporin 7 (GI 2350843; SEQ ID NO:41), produced using the
30 multisequence alignment program of LASERGENE software.

Figures 6A and 6B show the amino acid sequence alignment between MECHP-7 (2731369; SEQ ID NO:7) and mouse connexin 30.3 (GI 192647; SEQ ID NO:42), produced using the multisequence alignment program of LASERGENE software.

Figure 7 shows the amino acid sequence alignment between MECHP-16 (2069907; SEQ ID NO:16) and human beta subunit of Ca^{2+} activated K^{+} channel (GI 1055345; SEQ ID NO:43), produced using the multisequence alignment program of LASERGENE software.

Figures 8A and 8B show the amino acid sequence alignment between MECHP-17 (2243917; SEQ ID NO:17) and a homolog of Caenorhabditis elegans K^{+} channel protein (GI 3292929; SEQ ID NO:44), produced using the multisequence alignment program of LASERGENE software.

Figures 9A and 9B show the amino acid sequence alignment between MECHP-18 (2597476; SEQ ID NO:18) and human aquaporin 9 (GI 2887407; SEQ ID NO:45), produced using the multisequence alignment program of LASERGENE software.

Table 1 shows polypeptide and nucleotide sequence identification numbers (SEQ ID NOs), clone identification numbers (clone IDs), cDNA libraries, and cDNA fragments used to assemble full-length sequences encoding MECHP.

Table 2 shows features of each polypeptide sequence, including potential motifs, homologous sequences, and methods and algorithms used for identification of MECHP.

Table 3 shows the tissue-specific expression patterns of each nucleic acid sequence as determined by northern analysis, diseases, disorders, or conditions associated with these tissues, and the vector into which each cDNA was cloned.

Table 4 describes the tissues used to construct the cDNA libraries from which cDNA clones encoding MECHP were isolated.

Table 5 shows the tools, programs, and algorithms used to analyze MECHP, along with applicable descriptions, references, and threshold parameters.

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

10 DEFINITIONS

"MECHP" refers to the amino acid sequences of substantially purified MECHP obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and preferably the human species, from any source, whether natural, synthetic, semi-synthetic, or recombinant.

15 The term "agonist" refers to a molecule which, when bound to MECHP, increases or prolongs the duration of the effect of MECHP. Agonists may include proteins, nucleic acids, carbohydrates, or any other molecules which bind to and modulate the effect of MECHP.

An "allelic variant" is an alternative form of the gene encoding MECHP. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. Any given natural or recombinant gene may have none, one, or many allelic forms. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

25 "Altered" nucleic acid sequences encoding MECHP include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as MECHP or a polypeptide with at least one functional characteristic of MECHP. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding MECHP, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding MECHP. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent MECHP. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity,

hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of MECHP is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, positively charged amino acids may include lysine and arginine, and amino acids with uncharged polar head groups having similar hydrophilicity values
5 may include leucine, isoleucine, and valine; glycine and alanine; asparagine and glutamine; serine and threonine; and phenylalanine and tyrosine.

The terms "amino acid" and "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. In this context, "fragments," "immunogenic fragments," or "antigenic
10 fragments" refer to fragments of MECHP which are preferably at least 5 to about 15 amino acids in length, most preferably at least 14 amino acids, and which retain some biological activity or immunological activity of MECHP. Where "amino acid sequence" is recited to refer to an amino acid sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated
15 with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which, when bound to MECHP, decreases the
20 amount or the duration of the effect of the biological or immunological activity of MECHP. Antagonists may include proteins, nucleic acids, carbohydrates, antibodies, or any other molecules which decrease the effect of MECHP.

The term "antibody" refers to intact molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies
25 that bind MECHP polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin,
30 and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that fragment of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (given regions or three-dimensional structures on

the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition containing a nucleic acid sequence which is complementary to the "sense" strand of a specific nucleic acid sequence. Antisense molecules
5 may be produced by any method including synthesis or transcription. Once introduced into a cell, the complementary nucleotides combine with natural sequences produced by the cell to form duplexes and to block either transcription or translation. The designation "negative" can refer to the antisense strand, and the designation "positive" can refer to the sense strand.

The term "biologically active" refers to a protein having structural, regulatory, or
10 biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" refers to the capability of the natural, recombinant, or synthetic MECHP, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The terms "complementary" and "complementarity" refer to the natural binding of
15 polynucleotides by base pairing. For example, the sequence "5' A-G-T 3'" bonds to the complementary sequence "3' T-C-A 5'." Complementarity between two single-stranded molecules may be "partial," such that only some of the nucleic acids bind, or it may be "complete," such that total complementarity exists between the single stranded molecules. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength
20 of the hybridization between the nucleic acid strands. This is of particular importance in amplification reactions, which depend upon binding between nucleic acids strands, and in the design and use of peptide nucleic acid (PNA) molecules.

A "composition comprising a given polynucleotide sequence" and a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given
25 polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding MECHP or fragments of MECHP may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl),
30 detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

"Consensus sequence" refers to a nucleic acid sequence which has been resequenced to resolve uncalled bases, extended using the XL-PCR kit (Perkin-Elmer, Norwalk CT) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from the overlapping

sequences of more than one Incyte Clone using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI). Some sequences have been both extended and assembled to produce the consensus sequence.

5 The term "correlates with expression of a polynucleotide" indicates that the detection of the presence of nucleic acids, the same or related to a nucleic acid sequence encoding MECHP, by northern analysis is indicative of the presence of nucleic acids encoding MECHP in a sample, and thereby correlates with expression of the transcript from the polynucleotide encoding MECHP.

A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

10 The term "derivative" refers to the chemical modification of a polypeptide sequence, or a polynucleotide sequence. Chemical modifications of a polynucleotide sequence can include, for example, replacement of hydrogen by an alkyl, acyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any
15 similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

The term "similarity" refers to a degree of complementarity. There may be partial similarity or complete similarity. The word "identity" may substitute for the word "similarity." A partially complementary sequence that at least partially inhibits an identical sequence from
20 hybridizing to a target nucleic acid is referred to as "substantially similar." The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or northern blot, solution hybridization, and the like) under conditions of reduced stringency. A substantially similar sequence or hybridization probe will compete for and inhibit the binding of a completely similar (identical) sequence to the target
25 sequence under conditions of reduced stringency. This is not to say that conditions of reduced stringency are such that non-specific binding is permitted, as reduced stringency conditions require that the binding of two sequences to one another be a specific (i.e., a selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of complementarity (e.g., less than about 30% similarity or identity).
30 In the absence of non-specific binding, the substantially similar sequence or probe will not hybridize to the second non-complementary target sequence.

The phrases "percent identity" and "% identity" refer to the percentage of sequence similarity found in a comparison of two or more amino acid or nucleic acid sequences. Percent identity can be determined electronically, e.g., by using the MEGALIGN program (DNASTAR)

which creates alignments between two or more sequences according to methods selected by the user, e.g., the clustal method. (See, e.g., Higgins, D.G. and P.M. Sharp (1988) *Gene* 73:237-244.) Parameters for each method may be the default parameters provided by MEGALIGN or may be specified by the user. The clustal algorithm groups sequences into clusters by examining the distances between all pairs. The clusters are aligned pairwise and then in groups. The percentage similarity between two amino acid sequences, e.g., sequence A and sequence B, is calculated by dividing the length of sequence A, minus the number of gap residues in sequence A, minus the number of gap residues in sequence B, into the sum of the residue matches between sequence A and sequence B, times one hundred. Gaps of low or of no similarity between the two amino acid sequences are not included in determining percentage similarity. Percent identity between nucleic acid sequences can also be counted or calculated by other methods known in the art, e.g., the Jotun Hein method. (See, e.g., Hein, J. (1990) *Methods Enzymol.* 183:626-645.) Identity between sequences can also be determined by other methods known in the art, e.g., by varying hybridization conditions.

"Human artificial chromosomes" (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size, and which contain all of the elements required for stable mitotic chromosome segregation and maintenance.

The term "humanized antibody" refers to antibody molecules in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

"Hybridization" refers to any process by which a strand of nucleic acid binds with a complementary strand through base pairing.

The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C_0t or R_0t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively, to the sequence found in the naturally occurring molecule.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which

may affect cellular and systemic defense systems.

The term "microarray" refers to an arrangement of distinct polynucleotides on a substrate.

The terms "element" and "array element" in a microarray context, refer to hybridizable polynucleotides arranged on the surface of a substrate.

5 The term "modulate" refers to a change in the activity of MECHP. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of MECHP.

10 The phrases "nucleic acid" or "nucleic acid sequence," as used herein, refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material. In this context, "fragments" refers to those nucleic acid sequences which comprise a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:19-36, for example, as distinct from any other sequence in the same genome. For
15 example, a fragment of SEQ ID NO:19-36 is useful in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:19-36 from related polynucleotide sequences. A fragment of SEQ ID NO:19-36 is at least about 15-20 nucleotides in length. The precise length of the fragment of SEQ ID NO:19-36 and the region of SEQ ID NO:19-36 to which the fragment corresponds are routinely determinable by one of ordinary skill
20 in the art based on the intended purpose for the fragment. In some cases, a fragment, when translated, would produce polypeptides retaining some functional characteristic, e.g., antigenicity, or structural domain characteristic, e.g., ATP-binding site, of the full-length polypeptide.

25 The terms "operably associated" and "operably linked" refer to functionally related nucleic acid sequences. A promoter is operably associated or operably linked with a coding sequence if the promoter controls the translation of the encoded polypeptide. While operably associated or operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements, e.g., repressor genes, are not contiguously linked to the sequence encoding the polypeptide but still bind to operator sequences that control expression of the polypeptide.

30 The term "oligonucleotide" refers to a nucleic acid sequence of at least about 6 nucleotides to 60 nucleotides, preferably about 15 to 30 nucleotides, and most preferably about 20 to 25 nucleotides, which can be used in PCR amplification or in a hybridization assay or microarray. "Oligonucleotide" is substantially equivalent to the terms "amplimer," "primer," "oligomer," and "probe," as these terms are commonly defined in the art.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which

comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

5 The term "sample" is used in its broadest sense. A sample suspected of containing nucleic acids encoding MECHP, or fragments thereof, or MECHP itself, may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

10 The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, or an antagonist. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds
15 to the antibody.

 The term "stringent conditions" refers to conditions which permit hybridization between polynucleotides and the claimed polynucleotides. Stringent conditions can be defined by salt concentration, the concentration of organic solvent, e.g., formamide, temperature, and other conditions well known in the art. In particular, stringency can be increased by reducing the
20 concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature.

 The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least about 60% free, preferably about 75% free, and most preferably about 90% free from other components with
25 which they are naturally associated.

 A "substitution" refers to the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

 "Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers,
30 microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

 "Transformation" describes a process by which exogenous DNA enters and changes a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of

foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed" cells includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

A "variant" of MECHP polypeptides refers to an amino acid sequence that is altered by one or more amino acid residues. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties (e.g., replacement of leucine with isoleucine). More rarely, a variant may have "nonconservative" changes (e.g., replacement of glycine with tryptophan). Analogous minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, LASERGENE software (DNASTAR).

The term "variant," when used in the context of a polynucleotide sequence, may encompass a polynucleotide sequence related to MECHP. This definition may also include, for example, "allelic" (as defined above), "splice," "species," or "polymorphic" variants. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or an absence of domains. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

THE INVENTION

The invention is based on the discovery of new human membrane channel proteins (MECHP), the polynucleotides encoding MECHP, and the use of these compositions for the diagnosis, treatment, or prevention of cell proliferative, immune/inflammatory, transport/secretory, osmoregulatory, muscular, cardiovascular, and neurological disorders.

Table 1 lists the Incyte clones used to assemble full length nucleotide sequences encoding

MECHP. Columns 1 and 2 show the sequence identification numbers (SEQ ID NOs) of the polypeptide and nucleotide sequences, respectively. Column 3 shows the clone IDs of the Incyte clones in which nucleic acids encoding each MECHP were identified, and column 4 shows the cDNA libraries from which these clones were isolated. Column 5 shows Incyte clones and their
 5 corresponding cDNA libraries. Clones for which cDNA libraries are not indicated were derived from pooled cDNA libraries. The clones in column 5 were used to assemble the consensus nucleotide sequence of each MECHP and are useful as fragments in hybridization technologies.

The columns of Table 2 show various properties of each of the polypeptides of the invention: column 1 references the SEQ ID NO; column 2 shows the number of amino acid
 10 residues in each polypeptide; column 3 shows potential phosphorylation sites; column 4 shows potential glycosylation sites; column 5 shows the amino acid residues comprising signature sequences and motifs; column 6 shows the identity of each polypeptide; and column 7 shows analytical methods used to identify each polypeptide through sequence homology and protein motifs.

15 MECHP-1 has chemical and structural similarity with rat glutamic acid-rich protein (GI 2924369; SEQ ID NO:37). In particular, MECHP-1 and rat glutamic acid-rich protein share 15% overall identity. As shown in Figure 1, BLAST analysis identifies regions of MECHP-1 and rat glutamic acid-rich protein which share 27-30% identity. These regions extend from residue V12 through T163, P266 through G344, P461 through E548, and E653 through G709 in MECHP-1.

20 As shown in Figure 2, MECHP-2 has chemical and structural similarity with Drosophila voltage-gated potassium channel (GI 116443; SEQ ID NO:38) and P. penicillatus potassium channel α -subunit (GI 1763619; SEQ ID NO:39). In particular, MECHP-2 shares 18% identity with Drosophila voltage-gated K⁺ channel, and 17% identity with P. penicillatus K⁺ channel α -subunit. In particular, MECHP-2 shares 27% identity with Drosophila voltage-gated potassium
 25 channel and P. penicillatus potassium channel α -subunit over the first 133 residues, from M1 through T133 in MECHP-2.

As shown in Figures 3A and 3B, MECHP-3 has chemical and structural similarity with rat calcium-activated potassium channel rSK3 (GI 2564072; SEQ ID NO:40). In particular, MECHP-3 and rat rSK3 share 40% identity. MECHP-3 and rat rSK3 also share a canonical ion pore (P)
 30 region, including a GYG potassium ion selectivity sequence, from residue W192 through G213 in MECHP-3.

As shown in Figures 4A, 4B, and 4C, MECHP-4 has chemical and structural similarity with Drosophila voltage-gated potassium channel (GI 116443; SEQ ID NO:38) and P. penicillatus potassium channel α -subunit (GI 1763619; SEQ ID NO:39). In particular, MECHP-4 shares 28%

identity with Drosophila voltage-gated K⁺ channel, and 26% identity with P. penicillatus K⁺ channel α -subunit, respectively. MECHP-4, Drosophila voltage-gated K⁺ channel, and P. penicillatus K⁺ channel α -subunit also share a GYG potassium ion selectivity sequence from residue G372 through G374 in MECHP-4.

5 As shown in Figures 5A and 5B, MECHP-5 has chemical and structural similarity with rat aquaporin 7 (GI 2350843; SEQ ID NO:41). In particular, MECHP-5 and rat aquaporin 7 share 74% identity.

As shown in Figures 6A and 6B, MECHP-7 has chemical and structural similarity with mouse connexin 30.3 (GI 192647; SEQ ID NO:42). In particular, MECHP-7 and mouse connexin
10 30.3 (GI 192647) share 84% identity.

As shown in Figure 7, MECHP-16 has chemical and structural similarity with human beta subunit of Ca⁺ activated K⁺ channel (GI 1055345; SEQ ID NO:43). In particular, MECHP-16 and human beta subunit of Ca⁺ activated K⁺ channel share 40% identity.

As shown in Figures 8A and 8B, MECHP-17 has chemical and structural similarity with a
15 homolog of C. elegans K⁺ channel protein (GI 3292929; SEQ ID NO:44). In particular, MECHP-17 and the specified homolog of C. elegans K⁺ channel protein share 47% identity.

As shown in Figures 9A and 9B, MECHP-18 has chemical and structural similarity with human aquaporin 9 (GI 2887407; SEQ ID NO:45). In particular, MECHP-18 and human aquaporin 9 share 46% identity.

20 The columns of Table 3 show the tissue-specificity and diseases, disorders, or conditions associated with nucleotide sequences encoding MECHP. The first column of Table 3 lists the nucleotide SEQ ID NOs. Column 2 lists tissue categories which express MECHP as a fraction of total tissue categories expressing MECHP. Column 3 lists diseases, disorders, or conditions associated with those tissues expressing MECHP. Column 4 lists the vectors used to subclone the
25 cDNA library. Northern analysis shows the expression of SEQ ID NO:34 in only 7 libraries, of which 6 (86%) are associated with cell proliferation. Two of these libraries are associated with brain tissue, one with pancreatic islet cells, one with kidney tissue, one with fetal lung tissue, one with ovarian tissue, and one with adrenal tissue. Northern analysis shows the expression of SEQ ID NO:36 in only 3 libraries, one of which is associated with ovarian tumor tissue, one with
30 developing lung tissue, and one with gastrointestinal tissue associated with inflammation. Of particular note is the enriched expression of MECHP in neural and neuroendocrine tissue, most prominently the neural tissue-specific expression of SEQ ID NO:30.

The columns of Table 4 show descriptions of the tissues used to construct the cDNA libraries from which cDNA clones encoding MECHP were isolated. Column 1 references the

nucleotide SEQ ID NOs, column 2 shows the cDNA libraries from which these clones were isolated, and column 3 shows the tissue origins and other descriptive information relevant to the cDNA libraries in column 2.

The following fragments of the nucleotide sequences encoding MECHP are useful, for example, in hybridization or amplification technologies to identify SEQ ID NO:19-36, and to distinguish between SEQ ID NO:19-36 and related polynucleotide sequences. The useful fragments include the fragment of SEQ ID NO:19 from about nucleotide 764 to about nucleotide 808; the fragment of SEQ ID NO:20 from about nucleotide 523 to about nucleotide 582; the fragment of SEQ ID NO:21 from about nucleotide 628 to about nucleotide 669; the fragment of SEQ ID NO:22 from about nucleotide 779 to about nucleotide 826; the fragment of SEQ ID NO:23 from about nucleotide 64 to about nucleotide 108; the fragment of SEQ ID NO:24 from about nucleotide 1133 to about nucleotide 1180; the fragment of SEQ ID NO:25 from about nucleotide 656 to about nucleotide 700; the fragment of SEQ ID NO:26 from about nucleotide 153 to about nucleotide 197; the fragment of SEQ ID NO:27 from about nucleotide 2160 to about nucleotide 2219; the fragment of SEQ ID NO:28 from about nucleotide 1275 to about nucleotide 1322; the fragment of SEQ ID NO:29 from about nucleotide 313 to about nucleotide 348; the fragment of SEQ ID NO:30 from about nucleotide 994 to about nucleotide 1041; the fragment of SEQ ID NO:31 from about nucleotide 443 to about nucleotide 478; the fragment of SEQ ID NO:32 from about nucleotide 1175 to about nucleotide 1207; the fragment of SEQ ID NO:34 from about nucleotide 381 to about nucleotide 425; the fragment of SEQ ID NO:35 from about nucleotide 17 to about nucleotide 61; and the fragment of SEQ ID NO:36 from about nucleotide 54 to about nucleotide 98. The polypeptides encoded by the fragments of SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:35, AND SEQ ID NO:36 are useful, for example, as immunogenic peptides.

The invention also encompasses MECHP variants. A preferred MECHP variant is one which has at least about 80%, more preferably at least about 90%, and most preferably at least about 95% amino acid sequence identity to the MECHP amino acid sequence, and which contains at least one functional or structural characteristic of MECHP.

The invention also encompasses polynucleotides which encode MECHP. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:19-36, which encodes MECHP.

The invention also encompasses a variant of a polynucleotide sequence encoding MECHP. In particular, such a variant polynucleotide sequence will have at least about 70%, more

preferably at least about 85%, and most preferably at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding MECHP. A particular aspect of the invention encompasses a variant of a sequence selected from the group consisting of SEQ ID NO:19-36 which has at least about 70%, more preferably at least about 85%, and most preferably at least
5 about 95% polynucleotide sequence identity to a sequence selected from the group consisting of SEQ ID NO:19-36. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of MECHP.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding MECHP, some bearing minimal
10 similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring MECHP, and all such variations are to be
15 considered as being specifically disclosed.

Although nucleotide sequences which encode MECHP and its variants are preferably capable of hybridizing to the nucleotide sequence of the naturally occurring MECHP under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding MECHP or its derivatives possessing a substantially different codon usage,
20 e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding MECHP and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more
25 desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode MECHP and MECHP derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell
30 systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding MECHP or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:19-36, or to a fragment of SEQ ID NO:19-36, under various conditions of stringency. (See,

e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) For example, stringent salt concentration will ordinarily be less than about 750 mM NaCl and 75 mM trisodium citrate, preferably less than about 500 mM NaCl and 50 mM trisodium citrate, and most preferably less than about 250 mM NaCl and 25 mM trisodium citrate. Low stringency hybridization can be obtained in the absence of organic solvent, e.g., formamide, while high stringency hybridization can be obtained in the presence of at least about 35% formamide, and most preferably at least about 50% formamide. Stringent temperature conditions will ordinarily include temperatures of at least about 30°C, more preferably of at least about 37°C, and most preferably of at least about 42°C. Varying additional parameters, such as hybridization time, the concentration of detergent, e.g., sodium dodecyl sulfate (SDS), and the inclusion or exclusion of carrier DNA, are well known to those skilled in the art. Various levels of stringency are accomplished by combining these various conditions as needed. In a preferred embodiment, hybridization will occur at 30°C in 750 mM NaCl, 75 mM trisodium citrate, and 1% SDS. In a more preferred embodiment, hybridization will occur at 37°C in 500 mM NaCl, 50 mM trisodium citrate, 1% SDS, 35% formamide, and 100 µg/ml denatured salmon sperm DNA (ssDNA). In a most preferred embodiment, hybridization will occur at 42°C in 250 mM NaCl, 25 mM trisodium citrate, 1% SDS, 50 % formamide, and 200 µg/ml ssDNA. Useful variations on these conditions will be readily apparent to those skilled in the art.

The washing steps which follow hybridization can also vary in stringency. Wash stringency conditions can be defined by salt concentration and by temperature. As above, wash stringency can be increased by decreasing salt concentration or by increasing temperature. For example, stringent salt concentration for the wash steps will preferably be less than about 30 mM NaCl and 3 mM trisodium citrate, and most preferably less than about 15 mM NaCl and 1.5 mM trisodium citrate. Stringent temperature conditions for the wash steps will ordinarily include temperature of at least about 25°C, more preferably of at least about 42°C, and most preferably of at least about 68°C. In a preferred embodiment, wash steps will occur at 25°C in 30 mM NaCl, 3 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 42°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. In a most preferred embodiment, wash steps will occur at 68°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. Additional variations on these conditions will be readily apparent to those skilled in the art.

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Perkin-Elmer), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), r

combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the Robbins Hydra microdispenser (Robbins Scientific, Sunnyvale CA), Hamilton MICROLAB 2200 (Hamilton, Reno NV), Peltier Thermal
5 Cyclor 200 (PTC200; MJ Research, Watertown MA) and the ABI CATALYST 800 (Perkin-Elmer). Sequencing is then carried out using either ABI 373 or 377 DNA sequencing systems (Perkin-Elmer), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short
10 Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding MECHP may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which
15 may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See,
20 e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR.
25 Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available
30 software, such as OLIGO 4.06 primer analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include

sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to
5 analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Perkin-Elmer),
10 and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode MECHP may be cloned in recombinant DNA molecules that direct expression of
15 MECHP, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express MECHP.

The nucleotide sequences of the present invention can be engineered using methods
20 generally known in the art in order to alter MECHP-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create
25 new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

In another embodiment, sequences encoding MECHP may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucleic Acids Symp. Ser. 7:215-223, and Horn, T. et al. (1980) Nucleic Acids Symp. Ser.
30 7:225-232.) Alternatively, MECHP itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solid-phase techniques. (See, e.g., Roberge, J.Y. et al. (1995) Science 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (Perkin-Elmer). Additionally, the amino acid sequence of MECHP, or any part thereof, may be altered during direct synthesis and/or

combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) *Methods Enzymol.* 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY.)

In order to express a biologically active MECHP, the nucleotide sequences encoding MECHP or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding MECHP. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding MECHP. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding MECHP and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding MECHP and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding MECHP. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression

vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding MECHP. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding MECHP can be achieved using a multifunctional *E. coli* vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or pSPORT1 plasmid (Life Technologies). Ligation of sequences encoding MECHP into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for *in vitro* transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509.) When large quantities of MECHP are needed, e.g. for the production of antibodies, vectors which direct high level expression of MECHP may be used. For example, vectors containing the strong, inducible T5 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of MECHP. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast *Saccharomyces cerevisiae* or *Pichia pastoris*. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, *supra*; Bitter, G.A. et al. (1987) *Methods Enzymol.* 153:516-544; and Scorer, C.A. et al. (1994) *Bio/Technology* 12:181-184.)

Plant systems may also be used for expression of MECHP. Transcription of sequences encoding MECHP may be driven by viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., *The McGraw Hill Yearbook of Science and Technology* (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding MECHP may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses MECHP in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of MECHP in cell lines is preferred. For example, sequences encoding MECHP can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk* or *ap^r* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* or *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its

substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) *Methods Mol. Biol.* 55:121-131.)

5 Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding MECHP is inserted within a marker gene sequence, transformed cells containing sequences encoding MECHP can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence
10 encoding MECHP under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

 In general, host cells that contain the nucleic acid sequence encoding MECHP and that express MECHP may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR
15 amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

 Immunological methods for detecting and measuring the expression of MECHP using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such
20 techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on MECHP is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press,
25 St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

 A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled
30 hybridization or PCR probes for detecting sequences related to polynucleotides encoding MECHP include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding MECHP, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an

appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes,
5 fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding MECHP may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on
10 the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode MECHP may be designed to contain signal sequences which direct secretion of MECHP through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications
15 of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38), are available from
20 the American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding MECHP may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric MECHP
25 protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of MECHP activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding
30 peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A

fusion protein may also be engineered to contain a proteolytic cleavage site located between the MECHP encoding sequence and the heterologous protein sequence, so that MECHP may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch 10). A variety of
5 commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled MECHP may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract systems (Promega). These systems couple transcription and translation of protein-coding sequences
10 operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, preferably ³⁵S-methionine.

Fragments of MECHP may be produced not only by recombinant production, but also by direct peptide synthesis using solid-phase techniques. (See, e.g., Creighton, supra pp. 55-60.) Protein synthesis may be performed by manual techniques or by automation. Automated synthesis
15 may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin-Elmer). Various fragments of MECHP may be synthesized separately and then combined to produce the full length molecule.

THERAPEUTICS

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists
20 between regions of MECHP and human membrane channel proteins. In addition, the expression of MECHP is closely associated with nervous, reproductive, and gastrointestinal tissues; fetal development; and neurological, immune/inflammatory, and cell proliferative disorders, including cancer. Therefore, MECHP appears to play a role in cell proliferative, immune/inflammatory, transport/secretory, osmoregulatory, muscular, cardiovascular, and neurological disorders. In the
25 treatment of disorders associated with increased MECHP expression or activity, it is desirable to decrease the expression or activity of MECHP. In the treatment of disorders associated with decreased MECHP expression or activity, it is desirable to increase the expression or activity of MECHP.

Therefore, in one embodiment, MECHP or a fragment or derivative thereof may be
30 administered to a subject to treat or prevent a disorder associated with decreased expression or activity of MECHP. Examples of such disorders include, but are not limited to, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma,

- leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an
- 5 immune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus,
- 10 emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma,
- 15 Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a transport/secretory disorder such as akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, Bell's palsy,
- 20 Charcot-Marie Tooth disease, Chediak-Higashi syndrome, diabetes mellitus, diabetes insipidus, diabetic neuropathy, hyperkalemic periodic paralysis, normokalemic periodic paralysis, malignant hyperthermia, multidrug resistance, myotonic dystrophy, catatonia, dystonias, peripheral neuropathy, neurofibromatosis, postherpetic neuralgia, trigeminal neuropathy, sarcoidosis, sickle cell anemia, toxic shock syndrome, Wilson's disease, cataracts, infertility, pulmonary artery
- 25 stenosis, sensorineural autosomal deafness, hyperglycemia, hypoglycemia, goiter, Cushing's disease, glucose-galactose malabsorption syndrome, hypercholesterolemia, and allergies, including hay fever, asthma, and urticaria (hives); an osmoregulatory disorder such as diabetes insipidus, diarrhea, peritonitis, chronic renal failure, Addison's disease, SIADH, hypoaldosteronism, hyponatremia, adrenal insufficiency, hypothyroidism, hypernatremia,
- 30 hypokalemia, Barter's syndrome, metabolic acidosis, metabolic alkalosis, encephalopathy, edema, hypotension, and hypertension; a muscular disorder such as cardiomyopathy, myocarditis, Duchenne's muscular dystrophy, Becker's muscular dystrophy, myotonic dystrophy, central core disease, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, infectious myositis, polymyositis, dermatomyositis, inclusion body myositis, thyrotoxic myopathy,

and ethanol myopathy; a cardiovascular disorder such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery; congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, complications of cardiac transplantation; congenital lung anomalies, atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis, obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases, pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, pleural tumors, drug-induced lung disease, radiation-induced lung disease, and complications of lung transplantation; and a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Down syndrome, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease; prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome; fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases; neuromuscular disorders including spinal

muscular atrophy, carpal tunnel syndrome, mononeuritis multiplex; muscular dystrophies such as Duchenne's, myotonic facioscapulohumeral, oculopharyngeal, scapuloperoneal, congenital, distal, and ocular; congenital and metabolic myopathies, myotonia, peripheral nervous system disorders, dermatomyositis and polymyositis; inherited, metabolic, endocrine, and toxic myopathies;

5 myasthenia gravis, periodic paralysis; mental disorders including depression and bipolar disorder, and mood, anxiety, and schizophrenic disorders; seasonal affective disorder (SAD); akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, and Tourette's disorder; abnormalities in electrolytes such as calcium, phosphate, magnesium, and potassium; hypo- and hyperfunction of the thyroid, adrenal,

10 parathyroid, and pituitary; and primary and metastatic neoplasms.

In another embodiment, a vector capable of expressing MECHP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of MECHP including, but not limited to, those described above.

In a further embodiment, a pharmaceutical composition comprising a substantially

15 purified MECHP in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of MECHP including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of MECHP may be administered to a subject to treat or prevent a disorder associated with decreased expression or

20 activity of MECHP including, but not limited to, those listed above.

In a further embodiment, an antagonist of MECHP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of MECHP. Such disorders may include, but are not limited to, those discussed above. In one aspect, an antibody which specifically binds MECHP may be used directly as an antagonist or indirectly as a targeting

25 or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express MECHP.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding MECHP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of MECHP including, but not limited to, those described above.

30 In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment

or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of MECHP may be produced using methods which are generally known in the art. In particular, purified MECHP may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind MECHP. Antibodies to MECHP may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are especially preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with MECHP or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Cornebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to MECHP have an amino acid sequence consisting of at least about 5 amino acids, and, more preferably, of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein and contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of MECHP amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to MECHP may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. USA 80:2026-2030; and Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984)

Proc. Natl. Acad. Sci. USA 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce MECHP-specific single chain antibodies. Antibodies with related specificity, but of distinct
5 idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton D.R. (1991) Proc. Natl. Acad. Sci. USA 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents
10 as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. USA 86:3833-3837; Winter, G. et al. (1991) Nature 349:293-299.)

Antibody fragments which contain specific binding sites for MECHP may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing
15 the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) Science 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays
20 using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between MECHP and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering MECHP epitopes is preferred, but a competitive binding assay may also be employed (Pound, supra).

25 Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for MECHP. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of MECHP-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are
30 heterogeneous in their affinities for multiple MECHP epitopes, represents the average affinity, or avidity, of the antibodies for MECHP. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular MECHP epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} l/mole are preferred for use in immunoassays in which the MECHP-antibody complex must withstand

rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 l/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of MECHP, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and Cryer, A. (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is preferred for use in procedures requiring precipitation of MECHP-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding MECHP, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, the complement of the polynucleotide encoding MECHP may be used in situations in which it would be desirable to block the transcription of the mRNA. In particular, cells may be transformed with sequences complementary to polynucleotides encoding MECHP. Thus, complementary molecules or fragments may be used to modulate MECHP activity, or to achieve regulation of gene function. Such technology is now well known in the art, and sense or antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding MECHP.

Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. Methods which are well known to those skilled in the art can be used to construct vectors to express nucleic acid sequences complementary to the polynucleotides encoding MECHP. (See, e.g., Sambrook, supra; Ausubel, 1995, supra.)

Genes encoding MECHP can be turned off by transforming a cell or tissue with expression vectors which express high levels of a polynucleotide, or fragment thereof, encoding MECHP. Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more with a non-replicating vector, and may last even longer if appropriate replication elements are part of the vector system.

As mentioned above, modifications of gene expression can be obtained by designing

complementary sequences or antisense molecules (DNA, RNA, or PNA) to the control, 5', or regulatory regions of the gene encoding MECHP. Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, are preferred.

Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding MECHP.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding MECHP. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs

and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

- 5 Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al.
10 (1997) Nat. Biotech. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

- An additional embodiment of the invention relates to the administration of a
15 pharmaceutical or sterile composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of MECHP, antibodies to MECHP, and mimetics, agonists, antagonists, or inhibitors of MECHP. The compositions may be administered alone or in combination with at least one other agent, such as a stabilizing compound, which may be administered in any sterile, biocompatible
20 pharmaceutical carrier including, but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered to a patient alone, or in combination with other agents, drugs, or hormones.

- The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial,
25 intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

- In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used
30 pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA).

Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets,

pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combining active compounds with solid excipient and processing the resultant mixture of granules (optionally, after grinding) to obtain tablets or dragee cores. Suitable auxiliaries can be added, if desired. Suitable excipients include carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, and sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums, including arabic and tragacanth; and proteins, such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, and alginic acid or a salt thereof, such as sodium alginate.

Dragee cores may be used in conjunction with suitable coatings, such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with fillers or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations suitable for parenteral administration may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils, such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate, triglycerides, or liposomes. Non-lipid polycationic amino polymers may also be used for delivery. Optionally, the suspension may also contain suitable stabilizers or agents to increase the solubility of the compounds and allow for the preparation of highly concentrated solutions.

For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes.

The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, and succinic acids. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder which may contain any or all of the following: 1 mM to 50 mM histidine, 0.1% to 2% sucrose, and 2% to 7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of MECHP, such labeling would include amount, frequency, and method of administration.

Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells or in animal models such as mice, rats, rabbits, dogs, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example MECHP or fragments thereof, antibodies of MECHP, and agonists, antagonists or inhibitors of MECHP, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind MECHP may be used for the diagnosis of disorders characterized by expression of MECHP, or in assays to monitor patients being treated with MECHP or agonists, antagonists, or inhibitors of MECHP. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics.

Diagnostic assays for MECHP include methods which utilize the antibody and a label to detect MECHP in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring MECHP, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of MECHP expression. Normal or standard values for MECHP expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, preferably human, with antibody to MECHP under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, preferably by photometric means. Quantities of MECHP expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding MECHP may be

used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantitate gene expression in biopsied tissues in which expression of MECHP may be correlated with disease. The diagnostic assay may be used to determine absence,
5 presence, and excess expression of MECHP, and to monitor regulation of MECHP levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding MECHP or closely related molecules may be used to identify nucleic acid sequences which encode MECHP. The specificity
10 of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification (maximal, high, intermediate, or low), will determine whether the probe identifies only naturally occurring sequences encoding MECHP, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and should preferably
15 have at least 50% sequence identity to any of the MECHP encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:19-36 or from genomic sequences including promoters, enhancers, and introns of the gene encoding MECHP.

Means for producing specific hybridization probes for DNAs encoding MECHP include
20 the cloning of polynucleotide sequences encoding MECHP or MECHP derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ³²P or ³⁵S, or by enzymatic
25 labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding MECHP may be used for the diagnosis of disorders associated with expression of MECHP. Examples of such disorders include, but are not limited to, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis,
30 cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas,

- parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an immune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune
- 5 polyeocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis,
- 10 myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and
- 15 helminthic infections, and trauma; a transport/secretory disorder such as akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, Bell's palsy, Charcot-Marie Tooth disease, Chediak-Higashi syndrome, diabetes mellitus, diabetes insipidus, diabetic neuropathy, hyperkalemic periodic paralysis, normokalemic periodic paralysis, malignant hyperthermia, multidrug resistance, myotonic dystrophy, catatonia, dystonias, peripheral
- 20 neuropathy, neurofibromatosis, postherpetic neuralgia, trigeminal neuropathy, sarcoidosis, sickle cell anemia, toxic shock syndrome, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, sensorineural autosomal deafness, hyperglycemia, hypoglycemia, goiter, Cushing's disease, glucose-galactose malabsorption syndrome, hypercholesterolemia, and allergies, including hay fever, asthma, and urticaria (hives); an osmoregulatory disorder such as diabetes
- 25 insipidus, diarrhea, peritonitis, chronic renal failure, Addison's disease, SIADH, hypoaldosteronism, hyponatremia, adrenal insufficiency, hypothyroidism, hypernatremia, hypokalemia, Barter's syndrome, metabolic acidosis, metabolic alkalosis, encephalopathy, edema, hypotension, and hypertension; a muscular disorder such as cardiomyopathy, myocarditis, Duchenne's muscular dystrophy, Becker's muscular dystrophy, myotonic dystrophy, central core
- 30 disease, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, infectious myositis, polymyositis, dermatomyositis, inclusion body myositis, thyrotoxic myopathy, and ethanol myopathy; a cardiovascular disorder such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis,

balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery; congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic

5 heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, complications of cardiac transplantation; congenital lung anomalies, atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis,

10 obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases, pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis

15 obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, pleural tumors, drug-induced lung disease, radiation-induced lung disease, and complications of lung transplantation; and a neurological disorder such as

20 epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Down syndrome, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema,

25 epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease; prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome; fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the

30 central nervous system, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases; neuromuscular disorders including spinal muscular atrophy, carpal tunnel syndrome, mononeuritis multiplex; muscular dystrophies such as Duchenne's, myotonic facioscapulohumeral, oculopharyngeal, scapuloperoneal, congenital, distal, and ocular; congenital and metabolic myopathies, myotonia, peripheral nervous system disorders,

dermatomyositis and polymyositis; inherited, metabolic, endocrine, and toxic myopathies; myasthenia gravis, periodic paralysis; mental disorders including depression and bipolar disorder, and mood, anxiety, and schizophrenic disorders; seasonal affective disorder (SAD); akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, and Tourette's disorder; abnormalities in electrolytes such as calcium, phosphate, magnesium, and potassium; hypo- and hyperfunction of the thyroid, adrenal, parathyroid, and pituitary; and primary and metastatic neoplasms. The polynucleotide sequences encoding MECHP may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered MECHP expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding MECHP may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding MECHP may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding MECHP in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of MECHP, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding MECHP, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period

ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or over-expressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding MECHP may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding MECHP, or a fragment of a polynucleotide complementary to the polynucleotide encoding MECHP, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantitation of closely related DNA or RNA sequences.

Methods which may also be used to quantitate the expression of MECHP include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J. Immunol. Methods 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in an ELISA format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as targets in a microarray. The microarray can be used to monitor the expression level of large numbers of genes simultaneously and to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, and to develop and monitor the activities of therapeutic agents.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

In another embodiment of the invention, nucleic acid sequences encoding MECHP may be used to generate hybridization probes useful in mapping the naturally occurring genomic

sequence. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) site. Correlation between the location of the gene encoding MECHP on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The nucleotide sequences of the invention may be used to detect differences in gene sequences among normal, carrier, and affected individuals.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of a particular human chromosome is not known. New sequences can be assigned to chromosomal arms by physical mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the disease or syndrome has been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the subject invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, MECHP, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between MECHP and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test

compounds are synthesized on a solid substrate. The test compounds are reacted with MECHP, or fragments thereof, and washed. Bound MECHP is then detected by methods well known in the art. Purified MECHP can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding MECHP specifically compete with a test compound for binding MECHP. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with MECHP.

In additional embodiments, the nucleotide sequences which encode MECHP may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. [Attorney Docket No. PF-0589 P, filed September 2, 1998], U.S. Ser. No. [Attorney Docket No. PF-0632 P, filed November 12, 1998], U.S. Ser. No. [Attorney Docket No. PF-0648 P, filed December 9, 1998], U.S. Ser. No. [Attorney Docket No. PF-0664 P, filed January 26, 1999], and U.S. Ser. No. [Attorney Docket No. PF-0671 P, filed February 10, 1999], are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

RNA was purchased from Clontech or isolated from tissues described in Table 4. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA

purity. In some cases, RNA was treated with DNase. For most libraries, poly(A⁺) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the

5 POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel,

10 1997, supra, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative

15 agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUEScript plasmid (Stratagene), pSPORT1 plasmid (Life Technologies), or pINCY (Incyte Pharmaceuticals, Palo Alto CA). Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

20 II. Isolation of cDNA Clones

Plasmids were recovered from host cells by in vivo excision, using the UNIZAP vector system (Stratagene) or cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8

25 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and

30 thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a Fluoroskan II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

cDNA sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Perkin-Elmer) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing systems (Perkin-Elmer) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example V.

The polynucleotide sequences derived from cDNA sequencing were assembled and analyzed using a combination of software programs which utilize algorithms well known to those skilled in the art. Table 5 summarizes the tools, programs, and algorithms used and provides applicable descriptions, references, and threshold parameters. The first column of Table 5 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences). Sequences were analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polypeptide sequence alignments were generated using the default parameters specified by the clustal algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

The polynucleotide sequences were validated by removing vector, linker, and polyA sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The sequences were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS to acquire annotation using programs based on BLAST, FASTA, and BLIMPS. The sequences were assembled into full length polynucleotide sequences using programs based on Phred, Phrap, and Consed, and were screened for open

reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length amino acid sequences, and these full length sequences were subsequently analyzed by querying against databases such as the GenBank databases (described above), SwissProt, BLOCKS, PRINTS, Prosite, and Hidden Markov Model (HMM)-based protein family databases such as PFAM. HMM is a probabilistic approach which analyzes consensus primary structures of gene families. (See, e.g., Eddy, S.R. (1996) Curr. Opin. Struct. Biol. 6:361-365.)

The programs described above for the assembly and analysis of full length polynucleotide and amino acid sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:19-36. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies were described in The Invention section above.

IV. Northern Analysis

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in nucleotide databases such as GenBank or LIFESEQ (Incyte Pharmaceuticals, Palo Alto CA). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\% \text{ sequence identity} \times \% \text{ maximum BLAST score}}{100}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact within a 1% to 2% error, and, with a product score of 70, the match will be exact. Similar molecules are usually identified by selecting those which show product scores between 15 and 40, although lower scores may identify related molecules.

The results of northern analyses are reported as a percentage distribution of libraries in which the transcript encoding MECHP occurred. Analysis involved the categorization of cDNA libraries by organ/tissue and disease. The organ/tissue categories included cardiovascular, dermatologic, developmental, endocrine, gastrointestinal, hematopoietic/immune, musculoskeletal, nervous, reproductive, and urologic. The disease/condition categories included cancer,

inflammation/trauma, cell proliferation, neurological, and pooled. For each category, the number of libraries expressing the sequence of interest was counted and divided by the total number of libraries across all categories. Percentage values of tissue-specific and disease- or condition-specific expression are reported in the description of the invention.

5 **V. Extension of MECHP Encoding Polynucleotides**

The full length nucleic acid sequences of SEQ ID NO:19-36 was produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer, to initiate 3' extension of the known fragment. The initial primers were designed
10 using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one
15 extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg²⁺, (NH₄)₂SO₄, and β-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech),
20 ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2
25 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 μl PICO GREEN quantitation reagent (0.25% (v/v) PICO GREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 μl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was
30 scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μl to 10 μl aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates,

digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with *Pfu* DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulphoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer).

In like manner, the nucleotide sequence of SEQ ID NO:19-36 is used to obtain 5' regulatory sequences using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

VI. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:19-36 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 µCi of [³²P]-adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10⁷ counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon

membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under increasingly stringent conditions up to 0.1x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography and compared.

5 **VII. Microarrays**

A chemical coupling procedure and an ink jet device can be used to synthesize array elements on the surface of a substrate. (See, e.g., Baldeschweiler, supra.) An array analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced by
10 hand or using available methods and machines and contain any appropriate number of elements. After hybridization, nonhybridized probes are removed and a scanner used to determine the levels and patterns of fluorescence. The degree of complementarity and the relative abundance of each probe which hybridizes to an element on the microarray may be assessed through analysis of the scanned images.

15 Full-length cDNAs, Expressed Sequence Tags (ESTs), or fragments thereof may comprise the elements of the microarray. Fragments suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). Full-length cDNAs, ESTs, or fragments thereof corresponding to one of the nucleotide sequences of the present invention, or selected at random from a cDNA library relevant to the present invention, are
20 arranged on an appropriate substrate, e.g., a glass slide. The cDNA is fixed to the slide using, e.g., UV cross-linking followed by thermal and chemical treatments and subsequent drying. (See, e.g., Schena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645.) Fluorescent probes are prepared and used for hybridization to the elements on the substrate. The substrate is analyzed by procedures described above.

25 **VIII. Complementary Polynucleotides**

Sequences complementary to the MECHP-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring MECHP. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides
30 are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of MECHP. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the MECHP-encoding transcript.

IX. Expression of MECHP

Expression and purification of MECHP are achieved using bacterial or virus-based expression systems. For expression of MECHP in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*) hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express MECHP upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of MECHP in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding MECHP by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E. K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, MECHP is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from MECHP at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch 10 and 16). Purified MECHP obtained by these methods can be used directly in the following activity assay.

X. Demonstration of MECHP Activity

Aquaporin Activity of MECHP

Aquaporin activity of MECHP is demonstrated as the ability to induce osmotic water permeability in Xenopus laevis oocytes injected with MECHP cRNA (Ishibashi, K. et al. (1994)

Proc. Natl. Acad. Sci. USA 91:6269-6273). Oocytes injected with water are used as the control. Injected oocytes are given a hypotonic shock by being transferred from 200 mosM to 70 mosM modified Barth's buffer. The increase in osmotic volume of the oocytes, observed at 24°C by videomicroscopy, is proportional to the MECHP aquaporin activity in the injected oocytes.

5 Protein Transport Activity of MECHP

Protein transport activity of MECHP is demonstrated by its ability to catalyze the translocation of newly synthesized preprolactin into proteoliposomes in an in vitro system (Görlich, D. and T.A. Rapoport (1993) Cell 75:615-630). Proteoliposomes are prepared containing purified MECHP, purified dog Sec61p beta and gamma, purified dog SRP receptor, and a mixture of phospholipids (phosphatidylcholine, phosphatidylethanolamine, phosphatidylserine, and phosphatidylinositol) corresponding approximately to those found in native microsomes. The proteoliposomes are incubated in a wheat germ in vitro translation system in which a secretory protein (preprolactin) is synthesized in the presence of SRP and radioactive amino acids. After translation and synthesis of preprolactin, half of the sample is treated with 500 µg/ml proteinase K while the other half remains untreated. Any translocated preprolactin will be inaccessible to proteinase K while any untranslocated preprolactin will be degraded. The amount of preprolactin in the samples with and without proteinase K treatment is determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis followed by phosphor image analysis. The amount of preprolactin protected from proteinase K digestion in the proteinase K-treated sample is proportional to the protein transport activity of MECHP.

20 Gap Junction Activity of MECHP

Gap junction activity of MECHP is demonstrated as the ability to induce the formation of intercellular channels between paired Xenopus laevis oocytes injected with MECHP cRNA (Hennemann, supra). One week prior to the experimental injection with MECHP cRNA, oocytes are injected with antisense oligonucleotide to MECHP to reduce background. MECHP cRNA-injected oocytes are incubated overnight, stripped of vitelline membranes, and paired for recording of junctional currents by dual cell voltage clamp. The measured conductances are proportional to gap junction activity of MECHP.

25 Ion Channel Activity of MECHP

Ion channel activity of MECHP is demonstrated using an electrophysiological assay for ion conductance. MECHP can be expressed by transforming a mammalian cell line such as COS7, HeLa or CHO with a eukaryotic expression vector encoding MECHP. Eukaryotic expression vectors are commercially available, and the techniques to introduce them into cells are well known to those skilled in the art. A second plasmid which expresses any one of a number of

marker genes, such as β -galactosidase, is co-transformed into the cells to allow rapid identification of those cells which have taken up and expressed the foreign DNA. The cells are incubated for 48-72 hours after transformation under conditions appropriate for the cell line to allow expression and accumulation of MECHP and β -galactosidase.

5 Transformed cells expressing β -galactosidase are stained blue when a suitable colorimetric substrate is added to the culture media under conditions that are well known in the art. Stained cells are tested for differences in membrane conductance due to potassium ions by electrophysiological techniques that are well known in the art. Untransformed cells, and/or cells transformed with either vector sequences alone or β -galactosidase sequences alone, are used as
10 controls and tested in parallel. Cells expressing MECHP will have higher cation conductance relative to control cells. The contribution of MECHP to conductance can be confirmed by incubating the cells using antibodies specific for MECHP. The antibodies will bind to the extracellular side of MECHP, thereby blocking the pore in the ion channel, and the associated conductance.

15 Ion channel activity of MECHP is also measured as current flow across a MECHP-containing Xenopus oocyte membrane using the two-electrode voltage-clamp technique (Ishi et al., supra; Jegla, T. and L. Salkoff (1997) J. Neurosci. 17:32-44). MECHP is subcloned into an appropriate Xenopus oocyte expression vector, such as pBF, and 0.5-5 ng of mRNA is injected into mature stage IV oocytes. Injected oocytes are incubated at 18°C for 1-5 days. Inside-out
20 macropatches are excised into an intracellular solution containing 116 mM K-gluconate, 4 mM KCl, and 10 mM Hepes (pH 7.2). The intracellular solution is supplemented with varying concentrations of the MECHP mediator, such as cAMP, cGMP, or Ca^{+2} (in the form of CaCl_2), where appropriate. Electrode resistance is set at 2-5 M Ω and electrodes are filled with the intracellular solution lacking mediator. Experiments are performed at room temperature from a
25 holding potential of 0 mV. Voltage ramps (2.5 s) from -100 to 100 mV are acquired at a sampling frequency of 500 Hz. Current measured is proportional to the activity of MECHP in the assay.

XI. Functional Assays

MECHP function is assessed by expressing the sequences encoding MECHP at
30 physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 μg of recombinant vector are transiently transfected into a human cell line, preferably of endothelial or

hematopoietic origin, using either liposome formulations or electroporation. 1-2 µg of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP, and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of MECHP on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding MECHP and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding MECHP and other genes of interest can be analyzed by northern analysis or microarray techniques.

XII. Production of MECHP Specific Antibodies

MECHP substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the MECHP amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, ch. 11.)

Typically, oligopeptides 15 residues in length are synthesized using an ABI 431A peptide

synthesizer (Perkin-Elmer) using fmoc-chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, *supra*.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide activity by, for example, binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XIII. Purification of Naturally Occurring MECHP Using Specific Antibodies

Naturally occurring or recombinant MECHP is substantially purified by immunoaffinity chromatography using antibodies specific for MECHP. An immunoaffinity column is constructed by covalently coupling anti-MECHP antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing MECHP are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of MECHP (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/MECHP binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and MECHP is collected.

XIV. Identification of Molecules Which Interact with MECHP

MECHP, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton, A.E. and W.M. Hunter (1973) *Biochem. J.* 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled MECHP, washed, and any wells with labeled MECHP complex are assayed. Data obtained using different concentrations of MECHP are used to calculate values for the number, affinity, and association of MECHP with the candidate molecules.

25

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Table 1

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
1	19	1568324	UTRSNOT05	668081H1 (SCORNOT01), 777659H1 (COLNNOT05), 1419526F1 (KIDNNOT09), 1568324F6 (UTRSNOT05), 1568324H1 (UTRSNOT05), 1691082F6 (PROSTTUT10), 1866748F6 (SKINBIT01), 2133242H1 (ENDCNOT01), 2740849H1 (BRSTTUT14), 3488431H1 (EPIGNOT01), 3534835H1 (KIDNNOT25), 3556331H1 (LUNGNOT31), 3747086H1 (THYMNOT08)
2	20	4094907	BSCNS2T01	1298228F6 (BRSTNOT07), 1298228T6 (BRSTNOT07), 3518650T6 (LUNGNON03), 1673339T6 (BLADNOT05), 4094907H1 (BSCNSZT01), 810976R1 (LUNGNOT04)
3	21	518158	MMLR1DT01	518158H1 (MMLR1DT01), 1322305X302F1 (BLADNOT04), 1339742F1 (COLNTUT03), 1662883F6 (BRSTNOT09), 1868856F6 (SKINBIT01), 3329796H1 (HEAONOT04), SAPA00287F1
4	22	602926	BRSTTUT01	602926H1 (BRSTTUT01), 602926R1 (BRSTTUT01), 602926X15 (BRSTTUT01), 602926X18 (BRSTTUT01), 1236735H1 (LUNGFET03), 1294713F6 (PGANNOT03), 1342719X29R1 (COLNTUT03), 1796484T6 (PROSTTUT05)
5	23	922119	RATRN02	922119H1 (RATRN02), 2304391T6 (BRSTNOT05), 2925760H1 (SININOT04), 2925760T6 (SININOT04), 3283088H1 (HEAONOT05), 5330728H1 (DRGTNON04), 5343411H1 (CONENOT05)
6	24	2666782	THYMFET03	2666782H1 (THYMFET03), 2666782X305D2 (THYMFET03), 2666782X310F2 (THYMFET03), 2998445H1 (OVRTUT07), 2999052F6 (OVRTUT07), 3244028F6 (BRAINOT19), 3244028X317B2 (BRAINOT19)
7	25	2731369	OVRTUT04	2631755F6 (COLNTUT15), 2631755X300D1 (COLNTUT15), 2631755X303B1 (COLNTUT15), 2631755X303D1 (COLNTUT15), 2731369H1 (OVRTUT04), 2798719F6 (NPOLNOT01), 4406377H1 (PROSDIT01)

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
8	26	1375415	LUNGNOT10	664378R6 (SCORNOT01), 1375415H1 (LUNGNOT10), 1477459H1 (CORPNOT02), 3068750H1 (UTRSNOR01)
9	27	2733282	OVARTUT04	1821059F6 (GBLATUT01), 2620171R6 (KERANOT02), 2620171X306U2 (KERANOT02), 2733282F6 (OVARTUT04), 2733282H1 (OVARTUT04), 2733282X315F1 (OVARTUT04), 3618886F6 (EPIPNOT01), SBLA01906F1, SBLA01292F1
10	28	3148427	ADRENON04	3148427H1 (ADRENON04), 3877333F6 (HEARNOT06), 3877333T6 (HEARNOT06), 3877333X331B1 (HEARNOT06), 3877333X331U1 (HEARNOT06)
11	29	3342358	SPLNNOT09	259592X14 (HNT2RAT01), 2481052H1 (SMCANOT01), 3342358H1 (SPLNNOT09)
12	30	1267774	BRAINOT09	1267774F6 (BRAINOT09), 1267774H1 (BRAINOT09), 1740673R6 (HIPONON01), 1740673T6 (HIPONON01), 3242923H1 (BRAINOT19), 4837609H1 (BRAINOT01)
13	31	1817329	PROSNOT20	1817329F6 (PROSNOT20), 1817329H1 (PROSNOT20), 2506976F6 (CONUTUT01), 4313771F6 (BRAFNOT01), SAEA10065P1, SAEA02844F1, SAEA02136F1
14	32	3273307	PROSBPT06	2658420F6 (LUNGTUT09), 2658420X316D1 (LUNGTUT09), 2658420X325D1 (LUNGTUT09), 3273307F6 (PROSBPT06), 3273307H1 (PROSBPT06)
15	33	3824833	BRAXNOT01	3824833H1 (BRAXNOT01), SAGA02981F1, SAGA00581R1, SAGA01037F1
16	34	2069907	ISLTNOT01	2069907H1 (ISLTNOT01), 2069907X304D1 (ISLTNOT01), 2069907X313V1 (ISLTNOT01), 2736831F6 (OVARNOT09), 2736831T6 (OVARNOT09)
17	35	2243917	PANCTUT02	2243917H1 (PANCTUT02), 2243917F6 (PANCTUT02), 2108673R6 (BRAITUT03), 1804567F6 (SINTNOT13), 980106H1 (TONGTUT01)
18	36	2597476	OVARTUT02	2597476H1 (OVARTUT02), 2597476F6 (OVARTUT02), 1633918F6 (COLNNOT19), SAEC11415F1, SAEC10014F1, SBKA03380F1, SAEC10514F1

Table 2

SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
1	724	S123 S212 S246 S8 S20 S26 S32 T36 S38 T48 S73 S81 S82 S102 S161 S215 S227 S309 S375 T400 S492 S511 S545 S551 S564 S586 S627 T642 S119 S136 S152 S206 S240 S278 S424 S439 S444 S528 S539 S597 S607 T608 Y249	N582	ATP/GTP-binding site motif A (P-loop): A460-S467	Glutamic acid-rich protein (cyclic nucleotide-gated cation channel subunit)	BLAST MOTIFS
2	257	S162 S70 T93 T133 T242		Potassium channel signature: H74-T93	Potassium channel	MOTIFS PRINTS
3	377	S284 S174 S317 T101 T279 S338	N182 N334	Canonical ion pore region: W192-G213 Potassium channel signatures: T184-V206, G213-L239 Signal peptide: M1-S68 Transmembrane domains: W28-M46, I65-A81, L154-L173	Calcium-activated potassium channel	BLAST HMM MOTIFS PRINTS SPScan

Table 2 (cont.)

SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
4	491	S61 S144 S145 S150 S206 T274 S320 S463 S471 S472 T483 S75 T85 S118 T161 S183 T316 S489 Y437	N481 N487	Ion transport protein domain: C181-I405 Potassium channel signatures: E66-T85, P178-S206, G224-Q247, F250-L270, L294-S320, E323-E346, L354-T376, G383-F409 Potassium ion selectivity sequence: G372-G374 Transmembrane domain: V324-Y343	Voltage-gated potassium channel	BLAST HMM MOTIFS PFAM PRINTS
5	341	T189 S247 S9 Y292	N322	Major Intrinsic Protein (MIP): E26-Y271 Aquaporin NPA boxes: N93-A95, N225-S227 Transmembrane domain: M41-L59	Aquaporin	BLAST BLOCKS HMM MOTIFS PFAM PRINTS
6	476	T75 T105 T207 T222 S346 T378 S386 S71 T203 T224 S269 S309 Y235		Eubacterial secY protein: T75-I460 Signal peptide: M1-C46 Transmembrane domains: L33-F51, I147-L165, L239-I256	Sec61p alpha subunit	BLAST BLOCKS HMM MOTIFS PFAM PRINTS SPScan

Table 2 (cont.)

SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
7	266	S115 S121 T181	N119 N201	Connexin: M1-L208 Signal peptide: M1-A39 Transmembrane domain: I23-A39	Connexin	BLAST BLOCKS HMM MOTIFS ProfileScan PFAM PRINTS SPScan
8	182	S9 S130	N108	Transmembrane domains: R36-I55, A65-F84, V103-S130	Voltage-gated K ⁺ -channel (Plasmolipin)	BLAST HMM
9	942	S273 S302 S355 S368 T418 S419 S474 S498 T797 T2 T76 T92 S270 S318 S384 T557 T568 T593 T652 S685 T822 S823 S858 S927	N74 N97 N150 N231 N235 N253 N291 N521 N555 N579 N636 N821 N937	Signal peptide: M1-A31 Transmembrane domain: L900-L926	Calcium-dependent chloride channel (Lu-ECAM-1)	BLAST HMM SPScan
10	519	S74 S159 S187 T191 T224 T329 T441 S461 S466 S122 S172 T486 T516	N72 N215 N259 N394 N459	von Willebrand factor type A domain: D162-V337	L-type calcium channel subunit	BLAST PFAM PRINTS
11	251	S249 T52 T164 T182 S235 S35 S171	N50		Chloride intracellular channel (CLIC2)	BLAST

Table 2 (cont.)

SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
12	323	S173 T321 S44 S46 S165 S290 T50 S51 S169 T211 S228 S240	N48	PMP-22/PM20/EMP family protein: V8-Q207, T59-N72, Y176-D203 Signal peptide: M1-G29 Transmembrane domains: M10-V28, I106-A123, I134-S158, F180-V198	Voltage-gated Ca ²⁺ channel, gamma subunit	BLAST BLOCKS HMM MOTIFS PFAM SPScan
13	51	S5 T31			Ca ²⁺ channel, beta subunit	BLAST MOTIFS
14	113	S101 S102 T12 T46 T108 T65 S95 S96			Ca ²⁺ -activated K ⁺ channel	BLAST MOTIFS
15	215	T68 S106 S192 T198 T204	N42 N66 N74	Immunoglobulin domain: G43-I129 Myelin PO protein signature: L92-P119, D121-E150, A159-V183 Signal peptide: M1-S29 Transmembrane domain: T157-L177	Na ⁺ channel, beta subunit	BLAST HMM MOTIFS PFAM PRINTS SPScan

Table 2 (cont.)

SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
16	235	T36 S90 S122 S176 S6 S12 T135	N88 N96 N119	Transmembrane domain: I48-T68	Ca ²⁺ -activated K ⁺ channel, beta subunit	BLAST HMM MOTIFS
17	234	S29 S82 T174 T216 T57 S221	N130	Microbodies C-terminal targeting signal: S232-M234	K ⁺ channel protein	BLAST MOTIFS
18	301	T47 S286	N75 N128 N133	MIP family protein domain: R15-Y260 MIP family signature: H80-A88 Microbodies C-terminal targeting signal: C299-L301 Transmembrane domain: N54-Y71	Aquaporin 9	BLAST HMM MOTIFS PFAM

Table 3

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease, Disorder or Condition (Fraction of Total)	Vector
19	Reproductive Fetal	Cell Proliferative (0.570) Immune Response (0.210)	pINCY
20	Nervous Reproductive	Cell Proliferative (0.560) Immune Response (0.320)	pINCY
21	Reproductive Hematopoietic/Immune Gastrointestinal	Cell Proliferative (0.660) Immune Response (0.370)	PSPORT1
22	Reproductive Gastrointestinal Musculoskeletal	Cell Proliferative (0.790) Immune Response (0.210)	PSPORT1
23	Gastrointestinal (0.333) Reproductive (0.292) Cardiovascular (0.208)	Cell Proliferative and Cancer (0.625) Inflammation (0.500)	PSPORT1
24	Nervous (0.455) Reproductive (0.409)	Cell Proliferative and Cancer (0.591) Inflammation (0.273) Neurological (0.182)	pINCY
25	Nervous (0.400) Reproductive (0.400) Gastrointestinal (0.200)	Cell Proliferative and Cancer (0.800) Inflammation (0.200)	pINCY
26	Nervous (0.533) Gastrointestinal (0.133)	Cell Proliferative (0.533) Inflammation (0.267) Neurological (0.113)	pINCY
27	Reproductive (0.333) Dermatologic (0.167) Gastrointestinal (0.167)	Cell Proliferative (0.750)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease, Disorder or Condition (Fraction of Total)	Vector
28	Cardiovascular (0.250) Endocrine (0.250) Nervous (0.250)	Cancer (0.429) Trauma (0.429)	PSPORT1
29	Cardiovascular (0.500) Gastrointestinal (0.250) Hematopoietic/Immune (0.250)	Cancer (0.500) Inflammation (0.250)	pINCY
30	Nervous (1.000)	Inflammation (0.334) Neurological (0.167)	pINCY
31	Reproductive (0.500) Nervous (0.300) Gastrointestinal (0.200)	Cancer (0.600) Neurological (0.100)	pINCY
32	Reproductive (0.286) Endocrine (0.286)	Cancer (0.500) Inflammation (0.500)	pINCY
33	Nervous (0.667) Reproductive (0.333)	Cancer (0.333) Inflammation (0.333)	pINCY
34	Nervous (0.286)	Cell Proliferative (0.857)	pINCY
35	Nervous (0.296) Gastrointestinal (0.259) Reproductive (0.185)	Cell Proliferative (0.593) Inflammation/Immune Response (0.222)	pINCY
36	Reproductive (0.333) Cardiovascular (0.333) Gastrointestinal (0.333)	Cell Proliferative and Cancer (0.677) Inflammation (0.333)	pINCY

Table 4

Nucleotide SEQ ID NO:	Library	Library Comment
19	UTRSNOT05	Library was constructed using RNA isolated from the uterine tissue of a 45-year-old Caucasian female during a total abdominal hysterectomy and total colectomy. Pathology for the associated tumor tissue indicated multiple leiomyomas of the myometrium and a grade 2 colonic adenocarcinoma of the cecum. Patient history included multiple sclerosis and mitral valve disorder. Family history included type I diabetes, cerebrovascular disease, atherosclerotic coronary artery disease, malignant skin neoplasm, hypertension, and malignant neoplasm of the colon.
20	BSCNSZT01	Library was constructed using RNA isolated from diseased caudate nucleus tissue removed from the brain of a 49-year-old male. Patient history included schizophrenia.
21	MMLR1DT01	Library was constructed using RNA isolated from adherent mononuclear cells, which came from a pool of male and female donors. The cells were cultured for 24 hours following Ficoll Hypaque centrifugation.
22	BRSTTUT01	Library was constructed using RNA isolated from breast tumor tissue removed from a 55-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated invasive grade 4 mammary adenocarcinoma of mixed lobular and ductal type, extensively involving the left breast. Patient history included atrial tachycardia, blood in the stool, and a benign breast neoplasm. Family history included benign hypertension, atherosclerotic coronary artery disease, cerebrovascular disease, and depressive disorder.
23	RATRNOT02	Library was constructed using RNA isolated from the right atrium tissue of a 39-year-old Caucasian male, who died from a gunshot wound.
24	THYMFET03	Library was constructed using RNA isolated from thymus tissue removed from a Caucasian male fetus.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
25	OVRTUT04	Library was constructed using RNA isolated from ovarian tumor tissue removed from a 53-year-old Caucasian female during a total abdominal hysterectomy, removal of the fallopian tubes and ovaries, regional lymph node excision, peritoneal tissue destruction, and incidental appendectomy. Pathology indicated grade 1 transitional cell carcinoma of the right ovary. The left ovary had a hemorrhagic corpus luteum. The uterus had multiple leiomyomas (1 submucosal, 11 intramural), and the endometrium was inactive. The cul-de-sac contained abundant histiocytes and rare clusters of mesothelial cells. Patient history included breast fibrosclerosis and chronic stomach ulcer. Family history included acute stomach ulcer with perforation, breast cancer, bladder cancer, rectal/anal cancer, benign hypertension, coronary angioplasty, and hyperlipidemia.
26	LUNGNOT10	Library was constructed using RNA isolated from lung tissue of a Caucasian male fetus, who died at 23 weeks' gestation.
27	OVRTUT04	Library was constructed using RNA isolated from ovarian tumor tissue removed from a 53-year-old Caucasian female during a total abdominal hysterectomy, removal of the fallopian tubes and ovaries, regional lymph node excision, and peritoneal tissue destruction. Pathology indicated grade 1 transitional cell carcinoma of the right ovary. The left ovary had a hemorrhagic corpus luteum. The uterus had multiple leiomyomas (1 submucosal, 11 intramural), and the endometrium was inactive. The cul-de-sac contained abundant histiocytes and rare clusters of mesothelial cells. Patient history included breast fibrosclerosis and chronic stomach ulcer. Family history included acute stomach ulcer with perforation, breast cancer, bladder cancer, rectal/anal cancer, benign hypertension, coronary angioplasty, and hyperlipidemia.
28	ADRENON04	Library was constructed from 1.36 million independent clones from an adrenal tissue library. Starting RNA was made from adrenal gland tissue removed from a 20-year-old Caucasian male. The library was normalized in two rounds using conditions adapted from Soares et al. (Proc. Natl. Acad. Sci. USA (1994) 91:9228-9232) and Bonaldo et al. (Genome Res. (1996) 6:791-806), using a significantly longer (48-hours/round) reannealing hybridization period.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
29	SPLNOT09	Library was constructed using RNA isolated from diseased spleen tissue removed from a 22-year-old Caucasian male (Ashkenazi Jewish descent) during a total splenectomy. Pathology indicated Gaucher's disease with marked splenomegaly. Patient history included thyroid disorders and type 1 Gaucher's disease. Family history included benign hypertension, thyroid disease, myocardial infarction, cerebrovascular disease, arteriosclerotic cardiovascular disease, and prostate cancer.
30	BRAINOT09	Library was constructed using RNA isolated from brain tissue removed from a Caucasian male fetus, who died at 23 weeks' gestation.
31	PROSNOT20	Library was constructed using RNA isolated from diseased prostate tissue removed from a 65-year-old Caucasian male during a radical prostatectomy. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue indicated an adenocarcinoma.
32	PROSBPT06	Library was constructed using RNA isolated from diseased prostate tissue removed from a 66-year-old Caucasian male during a radical prostatectomy and lymph node excision. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue indicated grade 2 (of 4) adenocarcinoma, Gleason grade 3+3. The patient presented with elevated prostate specific antigen (PSA), proteinuria, decreased renal function, and urinary frequency. Patient history included hemiparesis, depressive disorder, sleep apnea, psoriasis, mitral valve prolapse, cerebrovascular disease, benign hypertension, and impotence. Family history included benign hypertension, cerebrovascular disease, and colon cancer.
33	BRAXNOT01	Library was constructed using RNA isolated from cerebellar tissue removed from a 70-year-old male. Patient history included chronic obstructive airways disease and left ventricular failure.
34	ISLTNOT01	Library was constructed using RNA isolated from a pooled collection of pancreatic islet cells.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
35	PANCUT02	Library was constructed using RNA isolated from pancreatic tumor tissue removed from a 45-year-old Caucasian female during radical pancreatic duodenectomy. Pathology indicated a grade 4 anaplastic carcinoma. Family history included benign hypertension, hyperlipidemia and atherosclerotic coronary artery disease.
36	OVARUT02	Library was constructed using RNA isolated from ovarian tumor tissue removed from a 51-year-old Caucasian female during an exploratory laparotomy, total abdominal hysterectomy, salpingo-oophorectomy, and an incidental appendectomy. Pathology indicated mucinous cystadenoma presenting as a multiloculated neoplasm involving the entire left ovary. The right ovary contained a follicular cyst and a hemorrhagic corpus luteum. The uterus showed proliferative endometrium and a single intramural leiomyoma. The peritoneal biopsy indicated benign glandular inclusions consistent with endosalpingiosis. Family history included atherosclerotic coronary artery disease, benign hypertension, breast cancer, and uterine cancer.

Table 5

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastm, blastx, tblastm, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25: 3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises as least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183: 63-98; and Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value= 1.0E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value= 1.0E-8 or less Full Length sequences: fastx score= 100 or greater
BLIMPS	A BLOCKS IMPROVED Searcher that matches a sequence against those in BLOCKS and PRINTS databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S and J.G. Henikoff, Nucl. Acid Res., 19:6565-72, 1991. J.G. Henikoff and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37: 417-424.	Score= 1000 or greater; Ratio of Score/Strength = 0.75 or larger; and Probability value= 1.0E-3 or less where applicable
PFAM	A Hidden Markov Models-based application useful for protein family search.	Krogh, A. et al. (1994) J. Mol. Biol., 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score= 10-50 bits, depending on individual protein families

Table 5 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25: 217-221.	Score= 4.0 or greater
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M. S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12: 431-439.	Score=5 or greater
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch et al. <i>supra</i> ; Wisconsin Package Program Manual, version 9, page MS1-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. A substantially purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:16, SEQ ID NO:17, and SEQ ID NO:18, and fragments thereof.
2. A substantially purified variant having at least 95% amino acid sequence identity to the amino acid sequence of claim 1.
3. An isolated and purified polynucleotide encoding the polypeptide of claim 1.
4. An isolated and purified polynucleotide variant having at least 95% polynucleotide sequence identity to the polynucleotide of claim 3.
5. An isolated and purified polynucleotide which hybridizes under stringent conditions to the polynucleotide of claim 3.
6. An isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide of claim 3.
7. A method for detecting a polynucleotide, the method comprising the steps of:
 - (a) hybridizing the polynucleotide of claim 6 to at least one nucleic acid in a sample, thereby forming a hybridization complex; and
 - (b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of the polynucleotide in the sample.
8. The method of claim 7 further comprising amplifying the polynucleotide prior to hybridization.
9. An isolated and purified polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:19-36 and fragments thereof.

10. An isolated and purified polynucleotide variant having at least 95% polynucleotide sequence identity to the polynucleotide of claim 9.

11. An isolated and purified polynucleotide having a sequence which is complementary to
5 the polynucleotide of claim 9.

12. An expression vector comprising at least a fragment of the polynucleotide of claim 3.

13. A host cell comprising the expression vector of claim 12.

10

14. A method for producing a polypeptide, the method comprising the steps of:

(a) culturing the host cell of claim 13 under conditions suitable for the expression of the polypeptide; and

(b) recovering the polypeptide from the host cell culture.

15

15. A pharmaceutical composition comprising the polypeptide of claim 1 in conjunction with a suitable pharmaceutical carrier.

16. A purified antibody which specifically binds to the polypeptide of claim 1.

20

17. A purified agonist of the polypeptide of claim 1.

18. A purified antagonist of the polypeptide of claim 1.

25

19. A method for treating or preventing a disorder associated with decreased expression or activity of MECHP, the method comprising administering to a subject in need of such treatment an effective amount of the pharmaceutical composition of claim 15.

20. A method for treating or preventing a disorder associated with increased expression or
30 activity of MECHP, the method comprising administering to a subject in need of such treatment an effective amount of the antagonist of claim 18.

12	VEPDPEAGSEQEVFSAVEGPSAEETPSDIESPEVLEIQDAHQGLLGMDPPGDMVDFVAA	1568324
	V P P ++ A P E P PE E Q + +P + AA	
8	VLPQPPGTPQKITEGAGRPQPEIESKPEANPOPEP-EVQPEPEPEP-EPEPEPEPAPEFAA	GI 2924369
72	ESTEDL---KALSSEEEEEEMGGAQEPESLLPPSVLDQASVIAERFVSFSRRSS-VAQE	1568324
	+ L + + E+ E G + QE + PP QA V V +R SS +	
66	PEVQITLPPPEPVEGEDVAEAGPSIQEIQEADPPQIPISQAQVA-----VWKVNRPPSSWMLSW	GI 2924369
128	DSKSSGFGSPRLVSRSSSVLSLEGSEKGLARHGSAT	1568324
	K P+ V SS +L E G + G+ T	
122	FWKGMKVVQPVPVYSSGGQNLAAHGCGPDQDGAQT	GI 2924369
461	PERDGKSPIVPCLOEEAGEPLGCKGRK-----PVLISLFDYEQIMAQE---HSPPKPSSAG	1568324
	P++DG PC + G G K P L L + +L ++ PP PS A	
150	PDQDGAQITLPEOGIGDPGSEDGSDKTSKIQDIEPSLMLLRMLEINLEKVLFPQPTPSQAW	GI 2924369
514	EMSPQORFFNP-PAVSQRITTSFGGRPSARSPLSPTE	1568324
	++ P+ P P + P PS +P P E	
210	KVEPEGAVLEPDPGTPMEVEPTENPSQNP-GPVE	GI 2924369
653	EKGPLPSPTAGLEESSGQGPSSPVALLQVQDFQQAEOQPKKEGSRDPADPSQOG	1568324
	E+ P P G + SS P PV L+ + + A QP G +PS G	
246	EEEPAAEIPQPGFQASSLPPRGDPVRLIEMWILHRLFWALPQPVLHGKAAEQEPSCPG	GI 2924369

FIGURE 1

2/16

1	M	S	R	P	L	I	T	R	S	P	A	S	-	-	-	-	-	-	-	P	L	N	N	Q	G	I	P	T	P	4094907	
1	M	A	S	-	V	A	A	W	L	P	F	A	R	A	A	A	I	G	W	V	P	I	A	T	H	P	L	P	P	P	GI 116443
1	M	N	G	D	I	G	A	W	I	S	C	A	R	T	A	G	I	G	W	V	P	I	S	S	K	E	-	P	S	A	GI 1763619
23	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4094907	
30	P	M	P	K	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 116443	
30	Y	L	N	K	Q	V	C	N	E	N	E	K	N	A	K	L	T	I	N	V	S	G	R	R	Y	Q	T	Y	S		GI 1763619
46	A	T	L	T	K	Y	P	E	S	R	I	G	R	L	F	D	G	T	E	P	I	V	L	-	D	S	L	K	Q	H	4094907
57	N	T	L	E	K	Y	P	D	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 116443	
60	H	T	L	R	K	F	K	E	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1763619	
75	Y	F	I	D	R	D	G	Q	M	F	R	Y	I	L	N	F	L	R	T	S	K	L	L	I	P	D	D	F	K	D	4094907
83	Y	F	F	D	R	D	P	D	I	F	R	H	I	L	N	Y	Y	R	T	G	K	L	H	Y	P	K	H	-	-	E	GI 116443
86	Y	Y	F	D	R	D	P	D	L	F	R	H	I	L	N	Y	Y	R	T	G	K	L	H	F	P	K	N	-	-	E	GI 1763619
105	Y	T	L	L	Y	E	E	A	-	K	Y	F	Q	L	Q	P	M	L	L	E	M	E	R	W	K	Q	D	R	E	T	4094907
111	C	L	T	S	Y	D	E	L	A	F	F	G	I	M	P	D	V	I	G	D	C	C	Y	E	D	Y	R	D	R	GI 116443	
114	C	V	S	S	F	E	D	E	L	T	F	F	G	I	K	G	F	N	I	N	N	C	C	W	D	D	Y	H	D	K	GI 1763619

FIGURE 2

3/16

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15  - - - R K R L L E Q E K S L A G W A L V L A G T G I G L M V 518158
271 L G H R R A L F E K R K R L S D Y A L I F G M F G I V V M V GI 2564072

42  L H A E M L W F G G C S W A L Y L F L V K C T I S I S T F L 518158
301 I E T E L S W G L Y S K D S M F S L A L K C L I S L S T I I GI 2564072

72  L L C L I V A F H A K E V Q L F M T D N G L R D W R V A L T 518158
331 L L G L I I A Y H T R E V Q L F V I D N G A D D W R I A M T GI 2564072

102 G R Q A A Q I V L E L V C G L H P A P V R - - - - - 518158
361 Y E R I L Y I S L E M L V C A I H P I P G E Y K F F W T A R GI 2564072

124 - - - - - G P P C V Q D L G A P L T S P Q P W P G F L G Q 518158
391 L A F S Y T P S R A E A D V D I I L S I P M F L R L Y L I A GI 2564072

148 G E A L L S L A M L - - - - - 518158
421 R V M L L H S K L F T D A S S R S I G A L N K I N F N T R F GI 2564072

158 - - - - - L L G L T L G L W L T T A W V L S 518158
451 V M K T L M T I C P G T V L L V F S I S L W I I A A W T V R GI 2564072

175 V A E R - - - - - Q A V N A T G H L S D T L W L I P I T F L T I G 518158
481 V C E R Y H D Q Q D V T S N F L G A M W L I S I T F L S I G GI 2564072

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FIGURE 3A

4/16

203	Y G D V V P G T M W G K I V C L C T G V M G V C C T A L L V	518158
511	Y G D M V P H T Y C G K G V C L L T G I M G A G C T A L V V	GI 2564072
233	A V V A R K L E F N K A E K H V H N F M M D I Q Y T K E M K	518158
541	A V V A R K L E L T K A E K H V H N F M M D T Q L T K R I K	GI 2564072
263	E S A A R V L Q E A W M F Y K H T R - - R K E S H A - A R R	518158
571	N A A A N V L R E T W L I Y K H T K L L K K I D H A K V R K	GI 2564072
290	H Q R K L L A A I N A F R Q V R L K H R K L R E Q V N S M V	518158
601	H Q R K F L Q A I H Q L R G V K M E Q R K L S D Q A N T L V	GI 2564072
320	D I S K M H M I L Y D L Q Q N L S S S H R A L E K Q I D T L	518158
631	D L S K M Q N V M Y D L I T E L N D R S E D L E K Q I G S L	GI 2564072
350	A G K L D A L T - - - - - - - - - - - - - - - E L L	518158
661	E S K L E H L T A S F N S L P L L I A D T L R Q Q Q Q L L	GI 2564072
361	S T A L G P R Q L P - - - - - - - - - - - - - - - E P S Q Q S K	518158
691	T A F V E A R G I S V A V G T S H A P P S D S P I G I S S T	GI 2564072
377		518158
721	S F P T P Y T S S S S C	GI 2564072

FIGURE 3B

6/16

151	L	F	E	K	E	L	E	K	F	D	T	L	R	F	G	Q	L	R	K	K	I	W	I	R	M	E	N	P	A	-	602926
170	M	G	I	D	V	Q	M	N	N	H	Q	A	K	-	-	N	F	R	Q	K	V	H	G	L	F	E	N	P	Q	S	GI 1763619
153	L	S	E	N	G	D	Q	N	L	Q	Q	L	T	-	-	N	M	R	Q	K	M	W	R	A	F	E	N	P	H	T	GI 116443
180	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	602926	
198	T	F	L	A	R	I	L	Y	I	T	G	F	F	I	A	V	S	V	G	S	T	I	I	E	T	I	D	-	-	GI 1763619	
181	S	T	S	A	L	V	F	Y	Y	V	T	G	F	F	I	A	V	S	V	M	A	N	V	V	E	T	V	P	-	-	GI 116443
203	C	V	H	S	M	S	E	F	Q	N	E	D	-	G	E	V	D	D	P	V	L	E	G	V	E	I	A	C	I	A	602926
226	C	S	A	N	R	-	-	-	-	-	-	-	P	C	G	E	V	Y	N	K	I	F	F	N	I	E	A	V	C	V	GI 1763619
209	C	G	H	R	P	G	R	A	G	T	L	P	C	G	E	R	Y	K	I	V	F	F	C	L	D	T	A	C	V	M	GI 116443
232	W	F	T	G	E	L	A	V	R	L	A	A	P	C	Q	K	K	F	W	K	N	P	L	N	I	I	D	F	V	602926	
250	V	F	T	I	E	Y	L	A	R	L	Y	S	A	P	C	R	F	R	H	A	R	I	S	L	S	I	I	D	V	I	GI 1763619
239	I	F	T	A	E	Y	L	L	R	L	F	A	A	P	D	R	C	K	F	V	R	S	V	M	S	I	I	D	V	V	GI 116443
262	S	I	I	P	F	Y	A	T	L	A	V	D	T	K	E	E	E	S	E	D	I	E	N	M	G	K	V	V	Q	I	602926
280	A	I	L	P	F	Y	I	G	L	A	M	T	-	K	T	S	I	S	G	A	F	V	S	-	-	-	-	-	-	-	GI 1763619
269	A	I	M	P	Y	Y	I	G	L	G	I	T	D	N	D	D	V	S	G	A	F	V	T	-	-	-	-	-	-	-	GI 116443
292	L	R	L	M	R	I	F	R	I	L	K	L	A	R	H	S	V	G	L	R	S	L	G	A	T	L	R	H	S	Y	602926
302	L	R	V	F	R	V	F	R	I	F	K	F	S	R	H	S	K	G	L	R	I	L	G	S	T	L	T	S	C	A	GI 1763619
292	L	R	V	F	R	V	F	R	I	F	K	F	S	R	H	S	Q	G	L	R	I	L	G	Y	T	L	K	S	C	A	GI 116443

FIGURE 4B

7/16

322	H	E	V	G	L	L	L	F	L	S	V	G	I	S	I	F	S	V	L	I	Y	S	V	E	K	D	D	H	T	602926	
332	S	E	L	G	F	L	L	F	S	L	S	M	A	I	I	I	F	A	T	V	V	F	Y	V	E	K	D	V	N	D	GI 1763619
322	S	E	L	G	F	L	V	F	S	L	A	M	A	I	I	I	F	A	T	V	M	F	Y	A	E	K	N	V	N	G	GI 116443
352	S	S	L	T	S	I	P	I	C	W	W	A	T	I	S	M	T	T	V	G	Y	G	D	T	H	P	V	T	L	602926	
362	S	D	F	T	S	I	P	A	S	F	W	Y	T	I	V	T	M	T	T	L	G	Y	G	D	M	V	P	K	T	I	GI 1763619
352	T	N	F	T	S	I	P	A	A	F	W	Y	T	I	V	T	M	T	T	L	G	Y	G	D	M	V	P	E	T	I	GI 116443
382	A	G	K	L	I	A	S	T	C	I	I	C	G	I	L	V	V	A	L	P	I	T	I	I	F	N	K	F	S	K	602926
392	P	G	K	L	V	G	S	I	C	S	L	S	G	V	L	V	I	A	L	P	V	P	V	I	V	S	N	F	S	R	GI 1763619
382	A	G	K	I	V	G	V	C	S	L	S	G	V	L	V	I	A	L	P	V	P	V	I	V	S	N	F	S	R	GI 116443	
412	Y	Y	Q	K	Q	K	D	I	D	V	D	Q	C	S	E	D	A	P	E	K	C	H	E	L	P	Y	F	N	I	R	602926
422	I	Y	L	Q	N	Q	R	A	D	K	R	R	A	N	Q	K	L	R	-	-	-	-	-	-	N	K	C	E	E	K	GI 1763619
412	I	Y	H	Q	N	Q	R	A	D	K	R	K	A	Q	R	K	A	R	L	A	R	I	R	I	A	K	A	S	S	G	GI 116443
442	D	I	Y	A	Q	R	M	H	A	F	I	T	S	L	S	S	V	G	I	V	S	D	P	D	S	T	D	A	S	602926	
446	E	E	-	-	-	K	K	K	-	-	E	S	S	E	T	V	T	R	F	I	I	S	N	Q	M	Y	-	-	-	GI 1763619	
442	A	A	F	V	S	K	K	K	A	A	E	A	R	W	A	A	Q	E	S	G	I	E	L	D	D	N	Y	R	D	E	GI 116443
472	S	I	E	D	N	E	D	I	C	N	T	T	S	L	E	N	C	T	A	K	602926										
468	T	I	F	S	M	K	F	A	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1763619	
472	D	I	F	E	L	Q	H	H	L	L	R	C	L	E	K	-	T	T	M	GI 116443											

FIGURE 4C

8/16

1	M	G	S	G	H	C	L	R	S	T	R	G	S	K	M	V	S	V	I	A	K	I	Q	E	I	L	Q	R	922119		
1	M	A	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	V	L	E	N	I	Q	S	V	L	Q	K	GI 2350843	
31	K	M	V	R	E	F	L	A	E	F	M	S	T	Y	V	M	M	V	F	G	L	G	S	V	A	H	M	V	L	N	922119
16	T	W	V	R	E	F	L	A	E	F	L	N	T	Y	V	L	M	V	F	G	L	G	S	V	A	H	M	V	L	G	GI 2350843
61	K	K	Y	G	S	Y	L	G	V	N	L	G	F	G	F	G	V	T	M	G	V	H	V	A	G	R	I	S	G	A	922119
46	E	R	L	G	S	Y	L	G	V	N	L	G	F	G	F	G	V	T	M	G	I	H	V	A	G	I	S	G	A	GI 2350843	
91	H	M	N	A	A	V	T	F	A	N	C	A	L	G	R	V	P	W	R	K	F	P	V	Y	V	L	G	Q	F	L	922119
76	H	M	N	P	A	V	T	F	T	N	C	A	L	G	R	M	A	G	R	K	F	P	I	Y	V	L	G	Q	F	L	GI 2350843
121	G	S	F	L	A	A	A	T	I	Y	S	L	F	Y	T	A	I	L	H	F	S	G	G	Q	L	M	V	T	G	P	922119
106	G	S	F	L	A	A	A	T	T	Y	L	I	F	Y	G	A	I	N	H	Y	A	G	E	T	L	L	V	T	G	P	GI 2350843
151	V	A	T	A	G	I	F	A	T	Y	L	P	D	H	M	T	L	W	R	G	F	L	N	E	A	W	L	T	G	M	922119
136	K	S	T	A	N	I	F	A	T	Y	L	P	E	H	M	T	L	W	R	G	F	V	D	E	V	F	V	T	G	M	GI 2350843
181	L	Q	L	C	L	F	A	I	T	D	Q	E	N	N	P	A	L	P	G	T	E	A	L	V	I	G	I	L	V	V	922119
166	L	Q	L	C	I	F	A	I	T	D	K	L	N	S	P	A	L	Q	G	T	E	P	L	M	I	G	I	L	V	C	GI 2350843
211	I	I	G	V	S	L	G	M	N	T	G	Y	A	I	N	P	S	R	D	L	P	P	R	I	F	T	F	I	A	G	922119
196	V	L	G	V	S	L	G	M	N	T	G	Y	A	I	N	P	S	R	D	L	P	P	R	F	F	T	F	I	A	G	GI 2350843

FIGURE 5A

9/16

241	W G K Q V F S N G E N W W V P V V A P L L G A Y L G G I I	922119
226	W G K K V F S A G N N W W V P V V A P L L G A Y L G G I V	GI 2350843
271	Y L V F I G S T I P R E P L K L E D S V A Y E D H G I T V L	922119
256	Y L G L I H A G I P P Q - - - - - - - - - - - - - - - -	GI 2350843
301	P K M G S H E P T I S P L T P V S V S P A N R S S V H P A P	922119
268	- - - - G S	GI 2350843
331	P L H E S M A L E H F	922119
269		GI 2350843

FIGURE 5B

10/16

1	M N W A F L Q G L L S G V N K Y S T V L S R I W L S V V F I	2731369
1	M N W G F L Q G I L S G V N K Y S T A L G R I W L S V V F I	GI 192647
31	F R V L V Y V V A A E E V W D D E Q K D F D C N T K Q P G C	2731369
31	F R V L V Y V V A A E E V W D D D Q K D F I C N T K Q P G C	GI 192647
61	T N V C Y D N Y F P I S N I R L W A L Q L I L V T C P S L L	2731369
61	P N V C Y D E F F P V S H V R L W A L Q L I L V T C P S L L	GI 192647
91	V V M H V A Y R E E R E R K H H L K H G P N A P S L Y D N L	2731369
91	V V M H V A Y R E E R E R K H R L K H G P N A P A L Y S N L	GI 192647
121	S K K R G G L W W T Y L L S L I F K A A V D A G F L Y I F H	2731369
121	S K K R G G L W W T Y L L S L I F K A A V D S G F L Y I F H	GI 192647
151	R L Y K D Y D M P R V V A C S V E P C P H T V D C Y I S R P	2731369
151	C I Y K D Y D M P R V V A C S V T P C P H T V D C Y I A R P	GI 192647
181	T E K K V F T Y F M V T T A A I C I L L N L S E V F Y L V G	2731369
181	T E K K V F T Y F M V V T A A I C I L L N L S E V V Y L V G	GI 192647

FIGURE 6A

11/16

211	K	R	C	M	E	I	F	G	P	R	H	R	R	P	R	C	R	E	C	L	P	D	T	C	P	P	Y	V	L	S	2731369
211	K	R	C	M	E	V	F	R	P	R	R	K	A	S	R	R	H	Q	L	P	D	T	C	P	P	Y	V	I	S	GI 192647	
241	Q	G	G	H	P	E	D	G	N	S	V	L	M	K	A	G	S	A	P	V	D	A	G	G	Y	P					2731369
241	K	G	G	H	P	Q	D	E	S	V	I	L	T	K	A	G	M	A	T	V	D	A	G	V	Y	P					GI 192647

FIGURE 6B

12/16

1	M	F	I	W	T	S	G	R	T	S	S	S	Y	R	H	D	E	K	R	N	I	Y	Q	K	I	R	D	H	D	L	2069907
1	M	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g1055345
31	L	D	K	R	K	T	V	T	A	L	K	A	G	E	D	R	A	I	L	L	G	L	A	M	M	V	C	S	I	M	2069907
3	-	-	-	K	K	L	V	M	A	Q	K	R	G	E	T	R	A	L	C	L	G	V	T	M	V	V	C	A	V	I	g1055345
61	M	Y	F	L	L	G	I	T	L	L	R	S	Y	M	Q	S	V	W	T	E	E	S	Q	C	T	L	L	N	A	S	2069907
30	T	Y	Y	I	L	V	T	V	L	P	L	Y	Q	K	S	V	W	T	Q	E	S	K	C	H	L	I	E	T	N	g1055345	
91	I	T	E	T	F	N	C	S	F	S	C	G	P	D	C	W	K	L	S	Q	Y	P	C	P	Q	V	Y	V	N	L	2069907
60	I	R	D	Q	E	E	-	-	-	-	-	L	K	G	K	K	V	P	Q	Y	P	C	-	-	L	W	V	N	V	g1055345	
121	T	S	S	G	E	K	L	L	Y	H	T	E	T	I	K	I	N	Q	K	C	S	Y	I	P	K	C	G	K	2069907		
82	S	A	A	G	R	W	A	V	L	Y	H	T	E	D	T	R	D	Q	N	Q	Q	C	S	Y	I	P	G	S	V	D	g1055345
151	N	F	E	E	S	M	S	L	V	N	V	M	E	N	F	R	K	Y	Q	H	F	S	C	Y	S	D	P	E	G	2069907	
112	N	Y	Q	T	A	R	A	D	V	E	K	V	R	A	K	F	Q	E	Q	Q	V	F	Y	C	F	S	A	P	R	G	g1055345
181	N	Q	K	S	V	I	L	T	K	L	Y	S	S	N	V	L	F	H	S	L	F	W	P	T	C	M	M	A	G	2069907	
142	N	E	T	S	V	L	F	Q	R	L	Y	G	P	Q	A	L	L	F	S	L	F	W	P	T	F	L	L	T	G	G	g1055345
211	V	A	I	V	A	M	V	K	L	T	Q	Y	L	S	L	L	C	E	R	I	Q	R	I	N	R	2069907					
172	L	L	I	I	A	M	V	K	S	N	Q	Y	L	S	I	L	A	A	Q	-	-	-	-	-	-	-	-	-	-	-	g1055345

FIGURE 7

13/16

FIGURE 8A

234 - - - - - 2243917
215 A T P T Q H Q L D A A K E A R A T A T S N T T N H T R S g3292929
234 - - - - - 2243917
245 D Q T Q P Q A Q I T H Q D Q P E S P K Q S P Q G D Y A S F A g3292929
234 - - - - - 2243917
275 F E T K L T G T A I R F S P L W P F C A L Y E V C A G V H g3292929
234 - - - - - 2243917
305 V F N L g3292929

14/16

FIGURE 8B

15/16

1	MVF	-	-	TQAPAEIMGHLRIRSL	LARQCLAEF	2597476
1	MQPEGA	EKGKSF	KQRL	VLKSS	SLAKETLS	g2887407
29	LGVFV	LL	LTQGA	VAAQAV	TSGETKGNFF	2597476
31	LGTF	IL	IVL	GCVC	VAAQAIL	g2887407
59	FLAGS	LAV	TAI	YVGGNV	SGAHLNPAFSLA	2597476
61	NVGF	SMA	VAM	AIYVAG	GVSGHINPAVSLA	g2887407
89	MCIVGR	LPW	VKKLP	IYILV	QLLSAF	2597476
91	MCLFGR	MKW	FKLP	FYVGA	QFLGAF	g2887407
119	YVLYH	DAL	QNYT	GGNLT	VTPKETASIFAT	2597476
121	FGI	YDGL	MSFA	GGL	LIVGENAT	g2887407
149	YPAPY	LSL	NNGF	LDQVL	GTGMLIVGLLAIL	2597476
151	YPAPY	LSL	ANAF	ADQVV	ATMILLIIVFAIF	g2887407
179	DRRNK	GVPA	GLEP	VVVG	MLILALGLSMGAN	2597476
181	DSRN	LGA	PRGLE	PIAIG	LLIIVIASLGLN	g2887407
209	CGI	PLNP	ARDL	GPRL	FTYVAGWGP	2597476
211	SGC	AMNP	ARDL	SPRL	FTALAGWGF	g2887407

FIGURE 9A

16/16

239	N	G	W	W	V	P	V	V	A	P	L	V	G	A	T	V	G	T	A	T	Y	Q	L	L	V	A	L	H	H	2597476	
241	N	N	F	W	W	I	P	V	V	G	P	L	V	G	A	V	I	G	L	I	Y	V	L	V	I	E	I	H	H	g2887407	
269	P	E	G	P	E	P	A	Q	D	L	V	S	A	Q	H	K	A	S	E	L	E	T	P	A	S	A	Q	M	L	E	2597476
271	P	E	-	P	D	S	V	F	K	A	E	Q	S	E	D	K	P	E	K	Y	E	-	-	-	-	-	-	-	L	S	g2887407
299	C	K	L																											2597476	
293	V	I	M																											g2887407	

FIGURE 9B

SEQUENCE LISTING

<110> INCYTE PHARMACEUTICALS, INC.

AU-YOUNG, Janice

BANDMAN, Olga

TANG, Y. Tom

REDDY, Roopa

HILLMAN, Jennifer L.

YUE, Henry

LAL, Preeti

CORLEY, Neil C.

GUEGLER, Karl J.

GORGONE, Gina

BAUGHN, Mariah R.

AZIMZAI, Yalda

<120> HUMAN MEMBRANE CHANNEL PROTEINS

<130> PF-0589 PCT

<140> To Be Assigned

<141> Herewith

<150> 09/145,815; unassigned; 09/191,283; unassigned; 09/208,821; unassigned
09/237,506; unassigned; 09/247,891; unassigned<151> 1998-09-02; 1998-09-02; 1998-11-12; 1998-11-12; 1998-12-09; 1998-12-09
1999-01-26; 1999-01-26; 1999-02-10; 1999-02-10

<160> 45

<170> PERL Program

<210> 1

<211> 724

<212> PRT

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 1568324CD1

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Met	Ser	Phe	Glu	Ser	Ile	Ser	Ser	Leu	Pro	Glu	Val	Glu	Pro	Asp
1				5					10					15
Pro	Glu	Ala	Gly	Ser	Glu	Gln	Glu	Val	Phe	Ser	Ala	Val	Glu	Gly
			20						25					30
Pro	Ser	Ala	Glu	Glu	Thr	Pro	Ser	Asp	Thr	Glu	Ser	Pro	Glu	Val
			35						40					45
Leu	Glu	Thr	Gln	Leu	Asp	Ala	His	Gln	Gly	Leu	Leu	Gly	Met	Asp
			50						55					60
Pro	Pro	Gly	Asp	Met	Val	Asp	Phe	Val	Ala	Ala	Glu	Ser	Thr	Glu
			65						70					75
Asp	Leu	Lys	Ala	Leu	Ser	Ser	Glu	Glu	Glu	Glu	Glu	Met	Gly	Gly
			80						85					90
Ala	Ala	Gln	Glu	Pro	Glu	Ser	Leu	Leu	Pro	Pro	Ser	Val	Leu	Asp

	95		100		105
Gln Ala Ser Val	Ile Ala Glu Arg Phe	Val Ser Ser Phe Ser	Arg		
	110		115		120
Arg Ser Ser Val	Ala Gln Glu Asp Ser	Lys Ser Ser Gly Phe	Gly		
	125		130		135
Ser Pro Arg Leu	Val Ser Arg Ser Ser	Ser Val Leu Ser Leu	Glu		
	140		145		150
Gly Ser Glu Lys	Gly Leu Ala Arg His	Gly Ser Ala Thr Asp	Ser		
	155		160		165
Leu Ser Cys Gln	Leu Ser Pro Glu Val	Asp Ile Ser Val Gly	Val		
	170		175		180
Ala Thr Glu Asp	Ser Pro Ser Val Asn	Gly Met Glu Pro Pro	Ser		
	185		190		195
Pro Gly Cys Pro	Val Glu Pro Asp Arg	Ser Ser Cys Lys Lys	Lys		
	200		205		210
Glu Ser Ala Leu	Ser Thr Arg Asp Arg	Leu Leu Leu Asp Lys	Ile		
	215		220		225
Lys Ser Tyr Tyr	Glu Asn Ala Glu His	His Asp Ala Gly Phe	Ser		
	230		235		240
Val Arg Arg Arg	Glu Ser Leu Ser Tyr	Ile Pro Lys Gly Leu	Val		
	245		250		255
Arg Asn Ser Ile	Ser Arg Phe Asn Ser	Leu Pro Arg Pro Asp	Pro		
	260		265		270
Glu Pro Val Pro	Pro Val Gly Ser Lys	Arg Gln Val Gly Ser	Arg		
	275		280		285
Pro Thr Ser Trp	Ala Leu Phe Glu Leu	Pro Gly Pro Ser Gln	Ala		
	290		295		300
Val Lys Gly Asp	Pro Pro Pro Ile Ser	Asp Ala Glu Phe Arg	Pro		
	305		310		315
Ser Ser Glu Ile	Val Lys Ile Trp Glu	Gly Met Glu Ser Ser	Gly		
	320		325		330
Gly Ser Pro Gly	Lys Gly Pro Gly Gln	Gly Gln Ala Asn Gly	Phe		
	335		340		345
Asp Leu His Glu	Pro Leu Phe Ile Leu	Glu Glu His Glu Leu	Gly		
	350		355		360
Ala Ile Thr Glu	Glu Ser Ala Thr Ala	Ser Pro Glu Ser Ser	Ser		
	365		370		375
Pro Thr Glu Gly	Arg Ser Pro Ala His	Leu Ala Arg Glu Leu	Lys		
	380		385		390
Glu Leu Val Lys	Glu Leu Ser Ser Ser	Thr Gln Gly Glu Leu	Val		
	395		400		405
Ala Pro Leu His	Pro Arg Ile Val Gln	Leu Ser His Val Met	Asp		
	410		415		420
Ser His Val Ser	Glu Arg Val Lys Asn	Lys Val Tyr Gln Leu	Ala		
	425		430		435
Arg Gln Tyr Ser	Leu Arg Ile Lys Ser	Asn Lys Pro Val Met	Ala		
	440		445		450
Arg Pro Pro Leu	Gln Trp Glu Lys Val	Ala Pro Glu Arg Asp	Gly		
	455		460		465
Lys Ser Pro Thr	Val Pro Cys Leu Gln	Glu Glu Ala Gly Glu	Pro		
	470		475		480
Leu Gly Gly Lys	Gly Lys Arg Lys Pro	Val Leu Ser Leu Phe	Asp		
	485		490		495
Tyr Glu Gln Leu	Met Ala Gln Glu His	Ser Pro Pro Lys Pro	Ser		
	500		505		510
Ser Ala Gly Glu	Met Ser Pro Gln Arg	Phe Phe Phe Asn Pro	Pro		

Ala Val Ser Gln	515	Arg Thr Thr Ser Pro	520	Gly Gly Arg Pro Ser	525
	530		535		540
Arg Ser Pro Leu	545	Ser Pro Thr Glu Thr	550	Phe Ser Trp Pro Asp	555
	560		565		570
Arg Glu Leu Cys	575	Ser Lys Tyr Ala Ser	580	Arg Asp Glu Ala Arg	585
	590		595		600
Ala Gly Gly Gly	605	Arg Pro Arg Gly Pro	610	Pro Val Asn Arg Ser	615
	620		625		630
Ser Val Pro Glu	635	Asn Met Val Glu Pro	640	Pro Leu Ser Gly Arg	645
	650		655		660
Gly Arg Cys Arg	665	Ser Leu Ser Thr Lys	670	Arg Gly Arg Gly Gly	675
	680		685		690
Glu Ala Ala Gln	695	Ser Pro Gly Pro Leu	700	Pro Gln Ser Lys Pro	705
	710		715		720
Gly Gly Glu Thr		Leu Tyr Val Thr Ala		Asp Leu Thr Leu Glu	
Asn Arg Arg Val		Ile Val Met Glu Lys		Gly Pro Leu Pro Ser	
Thr Ala Gly Leu		Glu Glu Ser Ser Gly		Gln Gly Pro Ser Ser	
Val Ala Leu Leu		Gly Gln Val Gln Asp		Phe Gln Gln Ser Ala	
Cys Gln Pro Lys		Glu Glu Gly Ser Arg		Asp Pro Ala Asp Pro	
Gln Gln Gly Arg		Val Arg Asn Leu Arg		Glu Lys Phe Gln Ala	
Asn Ser Val Gly					

<210> 2

<211> 257

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4094907CD1

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	5		10
Asn Gln Gly Ile Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala	20		30
	25		35
Pro Val His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu	35		45
	40		45
Ala Thr Leu Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe	50		60
	55		60
Asp Gly Thr Glu Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr	65		75
	70		75
Phe Ile Asp Arg Asp Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe	80		90
	85		90
Leu Arg Thr Ser Lys Leu Leu Ile Pro Asp Asp Phe Lys Asp Tyr	95		105
	100		105
Thr Leu Leu Tyr Glu Glu Ala Lys Tyr Phe Gln Leu Gln Pro Met	110		120
	115		120


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Leu Leu Glu Met Glu Arg Trp Lys Gln Asp Arg Glu Thr Gly Arg
      125      130      135
Phe Ser Arg Pro Cys Glu Cys Leu Val Val Arg Val Ala Pro Asp
      140      145      150
Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp Lys Ser Leu Ile Glu
      155      160      165
Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys Asn Ser Val Asn
      170      175      180
Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg Phe Pro Leu
      185      190      195
Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu Arg Leu
      200      205      210
Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly Val
      215      220      225
Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg
      230      235      240
Arg Thr Pro Arg Val Pro Ser Val Ile Arg Ile Lys Gln Glu Pro
      245      250      255
Leu Asp

```

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<210> 3
<211> 377
<212> PRT
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Incyte ID No: 518158CD1

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Met Gly Gly Asp Leu Val Leu Gly Leu Gly Ala Leu Arg Arg Arg
  1      5      10      15
Lys Arg Leu Leu Glu Gln Glu Lys Ser Leu Ala Gly Trp Ala Leu
      20      25      30
Val Leu Ala Gly Thr Gly Ile Gly Leu Met Val Leu His Ala Glu
      35      40      45
Met Leu Trp Phe Gly Gly Cys Ser Trp Ala Leu Tyr Leu Phe Leu
      50      55      60
Val Lys Cys Thr Ile Ser Ile Ser Thr Phe Leu Leu Leu Cys Leu
      65      70      75
Ile Val Ala Phe His Ala Lys Glu Val Gln Leu Phe Met Thr Asp
      80      85      90
Asn Gly Leu Arg Asp Trp Arg Val Ala Leu Thr Gly Arg Gln Ala
      95      100      105
Ala Gln Ile Val Leu Glu Leu Val Val Cys Gly Leu His Pro Ala
      110      115      120
Pro Val Arg Gly Pro Pro Cys Val Gln Asp Leu Gly Ala Pro Leu
      125      130      135
Thr Ser Pro Gln Pro Trp Pro Gly Phe Leu Gly Gln Gly Glu Ala
      140      145      150
Leu Leu Ser Leu Ala Met Leu Leu Leu Gly Leu Thr Leu Gly Leu
      155      160      165
Trp Leu Thr Thr Ala Trp Val Leu Ser Val Ala Glu Arg Gln Ala
      170      175      180
Val Asn Ala Thr Gly His Leu Ser Asp Thr Leu Trp Leu Ile Pro

```

Ile Thr Phe Leu	185	190	195
Thr Ile Gly Tyr Gly	200	Asp Val Val Pro Gly	Thr
Met Trp Gly Lys	215	220	225
Ile Val Cys Leu Cys	230	235	240
Leu Leu Val Ala Val	245	250	255
Cys Cys Thr Ala	260	265	270
Leu Leu Val Ala Arg	275	280	285
Lys Leu Glu	290	295	300
Phe Asn Lys Ala	305	310	315
Glu Lys His Val His	320	325	330
Asn Phe Met Met Asp	335	340	345
Ile	350	355	360
Gln Tyr Thr Lys	365	370	375
Glu Met Lys Glu Ser			
Ala Ala Arg Val Leu			
Gln			
Glu Ala Trp Met			
Phe Tyr Lys His Thr			
Arg Arg Lys Glu Ser			
His			
Ala Ala Arg Arg			
His Gln Arg Lys Leu			
Leu Leu Ala Ala Ile			
Asn Ala			
Phe Arg Gln Val			
Arg Leu Lys His Arg			
Lys Leu Arg Glu Gln			
Val			
Asn Ser Met Val			
Asp Ile Ser Lys Met			
His Met Ile Leu Tyr			
Asp			
Leu Gln Gln Asn			
Leu Ser Ser Ser His			
Arg Ala Leu Glu Lys			
Gln			
Ile Asp Thr Leu			
Ala Gly Lys Leu Asp			
Ala Leu Thr Glu Leu			
Leu			
Ser Thr Ala Leu			
Gly Pro Arg Gln Leu			
Pro Glu Pro Ser Gln			
Gln			
Ser Lys			

<210> 4

<211> 491

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 602926CD1

<400> 4

Met Val Phe Gly Glu	1	5	10	15
Phe Phe His Arg Pro Gly Gln Asp Glu Glu				
Leu Val Asn Leu Asn	20	25	30	35
Val Gly Gly Phe Lys Gln Ser Val Asp Gln				
Ser Thr Leu Leu Arg	35	40	45	50
Phe Pro His Thr Arg Leu Gly Lys Leu Leu				
Thr Cys His Ser Glu	50	55	60	65
Glu Ala Ile Leu Glu Leu Cys Asp Asp Tyr				
Ser Val Ala Asp Lys	65	70	75	80
Glu Tyr Tyr Phe Asp Arg Asn Pro Ser Ser				
Phe Arg Tyr Val Leu	80	85	90	95
Asn Phe Tyr Tyr Thr Gly Lys Leu His Val				
Met Glu Glu Leu Cys	95	100	105	110
Val Phe Ser Phe Cys Gln Glu Ile Glu Tyr				
Trp Gly Ile Asn Glu	110	115	120	125
Leu Phe Ile Asp Ser Cys Cys Ser Asn Arg				
Tyr Gln Glu Arg Lys	125	130	135	
Glu Glu Asn His Glu Lys Asp Trp Asp Gln				

Lys Ser His Asp Val Ser Thr Asp Ser Ser Phe Glu Glu Ser Ser	140	145	150
Leu Phe Glu Lys Glu Leu Glu Lys Phe Asp Thr Leu Arg Phe Gly	155	160	165
Gln Leu Arg Lys Lys Ile Trp Ile Arg Met Glu Asn Pro Ala Tyr	170	175	180
Cys Leu Ser Ala Lys Leu Ile Ala Ile Ser Ser Leu Ser Val Val	185	190	195
Leu Ala Ser Ile Val Ala Met Cys Val His Ser Met Ser Glu Phe	200	205	210
Gln Asn Glu Asp Gly Glu Val Asp Asp Pro Val Leu Glu Gly Val	215	220	225
Glu Ile Ala Cys Ile Ala Trp Phe Thr Gly Glu Leu Ala Val Arg	230	235	240
Leu Ala Ala Ala Pro Cys Gln Lys Lys Phe Trp Lys Asn Pro Leu	245	250	255
Asn Ile Ile Asp Phe Val Ser Ile Ile Pro Phe Tyr Ala Thr Leu	260	265	270
Ala Val Asp Thr Lys Glu Glu Glu Ser Glu Asp Ile Glu Asn Met	275	280	285
Gly Lys Val Val Gln Ile Leu Arg Leu Met Arg Ile Phe Arg Ile	290	295	300
Leu Lys Leu Ala Arg His Ser Val Gly Leu Arg Ser Leu Gly Ala	305	310	315
Thr Leu Arg His Ser Tyr His Glu Val Gly Leu Leu Leu Leu Phe	320	325	330
Leu Ser Val Gly Ile Ser Ile Phe Ser Val Leu Ile Tyr Ser Val	335	340	345
Glu Lys Asp Asp His Thr Ser Ser Leu Thr Ser Ile Pro Ile Cys	350	355	360
Trp Trp Trp Ala Thr Ile Ser Met Thr Thr Val Gly Tyr Gly Asp	365	370	375
Thr His Pro Val Thr Leu Ala Gly Lys Leu Ile Ala Ser Thr Cys	380	385	390
Ile Ile Cys Gly Ile Leu Val Val Ala Leu Pro Ile Thr Ile Ile	395	400	405
Phe Asn Lys Phe Ser Lys Tyr Tyr Gln Lys Gln Lys Asp Ile Asp	410	415	420
Val Asp Gln Cys Ser Glu Asp Ala Pro Glu Lys Cys His Glu Leu	425	430	435
Pro Tyr Phe Asn Ile Arg Asp Ile Tyr Ala Gln Arg Met His Ala	440	445	450
Phe Ile Thr Ser Leu Ser Ser Val Gly Ile Val Val Ser Asp Pro	455	460	465
Asp Ser Thr Asp Ala Ser Ser Ile Glu Asp Asn Glu Asp Ile Cys	470	475	480
Asn Thr Thr Ser Leu Glu Asn Cys Thr Ala Lys	485	490	

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<211> 341

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 922119CD1

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Val	Ser	Trp	Ser	Val	Ile	Ala	Lys	Ile	Gln	Glu	Ile	Leu	Gln	Arg	20	25	30	
Lys	Met	Val	Arg	Glu	Phe	Leu	Ala	Glu	Phe	Met	Ser	Thr	Tyr	Val	35	40	45	
Met	Met	Val	Phe	Gly	Leu	Gly	Ser	Val	Ala	His	Met	Val	Leu	Asn	50	55	60	
Lys	Lys	Tyr	Gly	Ser	Tyr	Leu	Gly	Val	Asn	Leu	Gly	Phe	Gly	Phe	65	70	75	
Gly	Val	Thr	Met	Gly	Val	His	Val	Ala	Gly	Arg	Ile	Ser	Gly	Ala	80	85	90	
His	Met	Asn	Ala	Ala	Val	Thr	Phe	Ala	Asn	Cys	Ala	Leu	Gly	Arg	95	100	105	
Val	Pro	Trp	Arg	Lys	Phe	Pro	Val	Tyr	Val	Leu	Gly	Gln	Phe	Leu	110	115	120	
Gly	Ser	Phe	Leu	Ala	Ala	Ala	Thr	Ile	Tyr	Ser	Leu	Phe	Tyr	Thr	125	130	135	
Ala	Ile	Leu	His	Phe	Ser	Gly	Gly	Gln	Leu	Met	Val	Thr	Gly	Pro	140	145	150	
Val	Ala	Thr	Ala	Gly	Ile	Phe	Ala	Thr	Tyr	Leu	Pro	Asp	His	Met	155	160	165	
Thr	Leu	Trp	Arg	Gly	Phe	Leu	Asn	Glu	Ala	Trp	Leu	Thr	Gly	Met	170	175	180	
Leu	Gln	Leu	Cys	Leu	Phe	Ala	Ile	Thr	Asp	Gln	Glu	Asn	Asn	Pro	185	190	195	
Ala	Leu	Pro	Gly	Thr	Glu	Ala	Leu	Val	Ile	Gly	Ile	Leu	Val	Val	200	205	210	
Ile	Ile	Gly	Val	Ser	Leu	Gly	Met	Asn	Thr	Gly	Tyr	Ala	Ile	Asn	215	220	225	
Pro	Ser	Arg	Asp	Leu	Pro	Pro	Arg	Ile	Phe	Thr	Phe	Ile	Ala	Gly	230	235	240	
Trp	Gly	Lys	Gln	Val	Phe	Ser	Asn	Gly	Glu	Asn	Trp	Trp	Trp	Val	245	250	255	
Pro	Val	Val	Ala	Pro	Leu	Leu	Gly	Ala	Tyr	Leu	Gly	Gly	Ile	Ile	260	265	270	
Tyr	Leu	Val	Phe	Ile	Gly	Ser	Thr	Ile	Pro	Arg	Glu	Pro	Leu	Lys	275	280	285	
Leu	Glu	Asp	Ser	Val	Ala	Tyr	Glu	Asp	His	Gly	Ile	Thr	Val	Leu	290	295	300	
Pro	Lys	Met	Gly	Ser	His	Glu	Pro	Thr	Ile	Ser	Pro	Leu	Thr	Pro	305	310	315	
Val	Ser	Val	Ser	Pro	Ala	Asn	Arg	Ser	Ser	Val	His	Pro	Ala	Pro	320	325	330	
Pro	Leu	His	Glu	Ser	Met	Ala	Leu	Glu	His	Phe					335	340		

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<211> 476

<212> PRT

<213> Homo sapiens

<220>
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 <223> Incyte ID No: 2666782CD1

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 Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Arg Glu
 20 25 30
 Lys Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys
 35 40 45
 Cys Gln Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp
 50 55 60
 Pro Phe Tyr Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr
 65 70 75
 Leu Met Glu Leu Gly Ile Ser Pro Ile Val Thr Ser Gly Leu Ile
 80 85 90
 Met Gln Leu Leu Ala Gly Ala Lys Ile Ile Glu Val Gly Asp Thr
 95 100 105
 Pro Lys Asp Arg Ala Leu Phe Asn Gly Ala Gln Lys Leu Phe Gly
 110 115 120
 Met Ile Ile Thr Ile Gly Gln Ala Ile Val Tyr Val Met Thr Gly
 125 130 135
 Met Tyr Gly Asp Pro Ala Glu Met Gly Ala Gly Ile Cys Leu Leu
 140 145 150
 Ile Ile Ile Gln Leu Phe Val Thr Ser Leu Ile Val Leu Leu Leu
 155 160 165
 Asp Glu Leu Leu Gln Thr Gly Tyr Ser Leu Gly Ser Gly Ile Ser
 170 175 180
 Leu Val Ile Ala Thr Asn Ile Cys Glu Thr Ile Val Trp Lys Ala
 185 190 195
 Phe Ser Pro Thr Thr Ile Asn Thr Gly Arg Gly Thr Glu Phe Glu
 200 205 210
 Gly Ala Val Ile Ala Leu Phe His Leu Leu Ala Thr Arg Thr Asp
 215 220 225
 Lys Val Arg Ala Leu Arg Glu Ala Phe Tyr Arg Gln Asn Leu Pro
 230 235 240
 Asn Leu Met Asn Leu Ile Ala Thr Val Phe Val Phe Ala Val Val
 245 250 255
 Ile Tyr Phe Gln Gly Phe Arg Val Asp Leu Pro Ile Lys Ser Ala
 260 265 270
 Arg Tyr Arg Gly Gln Tyr Ser Ser Tyr Pro Ile Lys Leu Phe Tyr
 275 280 285
 Thr Ser Asn Ile Pro Ile Ile Leu Gln Ser Ala Leu Val Ser Asn
 290 295 300
 Leu Tyr Val Ile Ser Gln Met Leu Ser Val Arg Phe Ser Gly Asn
 305 310 315
 Phe Leu Val Asn Leu Leu Gly Gln Trp Ala Asp Val Ser Gly Gly
 320 325 330
 Gly Pro Ala Arg Ser Tyr Pro Val Gly Gly Leu Cys Tyr Tyr Leu
 335 340 345
 Ser Pro Pro Glu Ser Met Gly Ala Ile Phe Glu Asp Pro Val His
 350 355 360
 Val Val Val Tyr Ile Ile Phe Met Leu Gly Ser Cys Ala Phe Phe
 365 370 375
 Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val

	380		385		390
Ala Lys Gln Leu	Lys Glu Gln Gln Met	Val Met Arg Gly His	Arg		
	395		400		405
Asp Thr Ser Met	Val His Glu Leu Asn	Arg Tyr Ile Pro Thr	Ala		
	410		415		420
Ala Ala Phe Gly	Gly Leu Cys Ile Gly	Ala Leu Ser Val Leu	Ala		
	425		430		435
Asp Phe Leu Gly	Ala Ile Gly Ser Gly	Thr Gly Ile Leu Leu	Ala		
	440		445		450
Val Thr Ile Ile	Tyr Gln Tyr Phe Glu	Ile Phe Val Lys Glu	Gln		
	455		460		465
Ala Glu Val Gly	Gly Met Gly Ala Leu	Phe Phe			
	470		475		

<210> 7

<211> 266

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2731369CD1

<400> 7

Met Asn Trp Ala Phe	Leu Gln Gly Leu	Leu Ser Gly Val	Asn Lys
1	5	10	15
Tyr Ser Thr Val Leu	Ser Arg Ile Trp	Leu Ser Val Val	Phe Ile
	20	25	30
Phe Arg Val Leu Val	Tyr Val Val Ala	Ala Glu Glu Val	Trp Asp
	35	40	45
Asp Glu Gln Lys Asp	Phe Asp Cys Asn	Thr Lys Gln Pro	Gly Cys
	50	55	60
Thr Asn Val Cys Tyr	Asp Asn Tyr Phe	Pro Ile Ser Asn	Ile Arg
	65	70	75
Leu Trp Ala Leu Gln	Leu Ile Leu Val	Thr Cys Pro Ser	Leu Leu
	80	85	90
Val Val Met His Val	Ala Tyr Arg Glu	Glu Arg Glu Arg	Lys His
	95	100	105
His Leu Lys His Gly	Pro Asn Ala Pro	Ser Leu Tyr Asp	Asn Leu
	110	115	120
Ser Lys Lys Arg Gly	Gly Leu Trp Trp	Thr Tyr Leu Leu	Ser Leu
	125	130	135
Ile Phe Lys Ala Ala	Val Asp Ala Gly	Phe Leu Tyr Ile	Phe His
	140	145	150
Arg Leu Tyr Lys Asp	Tyr Asp Met Pro	Arg Val Val Ala	Cys Ser
	155	160	165
Val Glu Pro Cys Pro	His Thr Val Asp	Cys Tyr Ile Ser	Arg Pro
	170	175	180
Thr Glu Lys Lys Val	Phe Thr Tyr Phe	Met Val Thr Thr	Ala Ala
	185	190	195
Ile Cys Ile Leu Leu	Asn Leu Ser Glu	Val Phe Tyr Leu	Val Gly
	200	205	210
Lys Arg Cys Met Glu	Ile Phe Gly Pro	Arg His Arg Arg	Pro Arg
	215	220	225
Cys Arg Glu Cys Leu	Pro Asp Thr Cys	Pro Pro Tyr Val	Leu Ser

	230		235		240
Gln Gly Gly His	Pro Glu Asp Gly Asn	Ser Val Leu Met Lys	Ala		
	245		250		255
Gly Ser Ala Pro	Val Asp Ala Gly Gly	Tyr Pro			
	260		265		

<210> 8

<211> 182

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1375415CD1

<400> 8

Met Ala Glu Phe Pro Ser Lys Val Ser Thr Arg Thr Ser Ser Pro		
1	5	10 15
Ala Gln Gly Ala Glu Ala Ser Val Ser Ala Leu Arg Pro Asp Leu		
	20 25	30
Gly Phe Val Arg Ser Arg Leu Gly Ala Leu Met Leu Leu Gln Leu		
	35 40	45
Val Leu Gly Leu Leu Val Trp Ala Leu Ile Ala Asp Thr Pro Tyr		
	50 55	60
His Leu Tyr Pro Ala Tyr Gly Trp Val Met Phe Val Ala Val Phe		
	65 70	75
Leu Trp Leu Val Thr Ile Val Leu Phe Asn Leu Tyr Leu Phe Gln		
	80 85	90
Leu His Met Lys Leu Tyr Met Val Pro Trp Pro Leu Val Leu Met		
	95 100	105
Ile Phe Asn Ile Ser Ala Thr Val Leu Tyr Ile Thr Ala Phe Ile		
	110 115	120
Ala Cys Ser Ala Ala Val Asp Leu Thr Ser Leu Arg Gly Thr Arg		
	125 130	135
Pro Tyr Asn Gln Arg Ala Ala Ala Ser Phe Phe Ala Cys Leu Val		
	140 145	150
Met Ile Ala Tyr Gly Val Ser Ala Phe Phe Ser Tyr Gln Ala Trp		
	155 160	165
Arg Gly Val Gly Ser Asn Ala Ala Thr Ser Gln Met Ala Gly Gly		
	170 175	180
Tyr Ala		

<210> 9

<211> 942

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2733282CD1

<400> 9

Met Thr Gln Arg Ser Ile Ala Gly Pro Ile Cys Asn Leu Lys Phe		
1	5	10 15

Val Thr Leu Leu Val Ala Leu Ser Ser Glu Leu Pro Phe Leu Gly	20	25	30
Ala Gly Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile	35	40	45
Ala Ile Asn Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn	50	55	60
Ile Lys Glu Met Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala	65	70	75
Thr Lys Arg Arg Val Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro	80	85	90
Ala Thr Trp Lys Ala Asn Asn Asn Ser Lys Ile Lys Gln Glu Ser	95	100	105
Tyr Glu Lys Ala Asn Val Ile Val Thr Asp Trp Tyr Gly Ala His	110	115	120
Gly Asp Asp Pro Tyr Thr Leu Gln Tyr Arg Gly Cys Gly Lys Glu	125	130	135
Gly Lys Tyr Ile His Phe Thr Pro Asn Phe Leu Leu Asn Asp Asn	140	145	150
Leu Thr Ala Gly Tyr Gly Ser Arg Gly Arg Val Phe Val His Glu	155	160	165
Trp Ala His Leu Arg Trp Gly Val Phe Asp Glu Tyr Asn Asn Asp	170	175	180
Lys Pro Phe Tyr Ile Asn Gly Gln Asn Gln Ile Lys Val Thr Arg	185	190	195
Cys Ser Ser Asp Ile Thr Gly Ile Phe Val Cys Glu Lys Gly Pro	200	205	210
Cys Pro Gln Glu Asn Cys Ile Ile Ser Lys Leu Phe Lys Glu Gly	215	220	225
Cys Thr Phe Ile Tyr Asn Ser Thr Gln Asn Ala Thr Ala Ser Ile	230	235	240
Met Phe Met Gln Ser Tyr Leu Cys Gly Glu Ile Cys Asn Ala Ser	245	250	255
Thr His Asn Gln Glu Ala Pro Asn Leu Gln Asn Gln Met Cys Ser	260	265	270
Leu Arg Ser Ala Trp Asp Val Ile Thr Asp Ser Ala Asp Phe His	275	280	285
His Ser Phe Pro Met Asn Gly Thr Glu Leu Pro Pro Pro Pro Thr	290	295	300
Phe Ser Leu Val Glu Ala Gly Asp Lys Val Val Cys Leu Val Leu	305	310	315
Asp Val Ser Ser Lys Met Ala Glu Ala Asp Arg Leu Leu Gln Leu	320	325	330
Gln Gln Ala Ala Glu Phe Tyr Leu Met Gln Ile Val Glu Ile His	335	340	345
Thr Phe Val Gly Ile Ala Ser Phe Asp Ser Lys Gly Glu Ile Arg	350	355	360
Ala Gln Leu His Gln Ile Asn Ser Asn Asp Asp Arg Lys Leu Leu	365	370	375
Val Ser Tyr Leu Pro Thr Thr Val Ser Ala Lys Thr Asp Ile Ser	380	385	390
Ile Cys Ser Gly Leu Lys Lys Gly Phe Glu Val Val Glu Lys Leu	395	400	405
Asn Gly Lys Ala Tyr Gly Ser Val Met Ile Leu Val Thr Ser Gly	410	415	420
Asp Asp Lys Leu Leu Gly Asn Cys Leu Pro Thr Val Leu Ser Ser	425	430	435

Gly Ser Thr Ile	His Ser Ile Ala Leu	Gly Ser Ser Ala Ala	Pro
440	445		450
Asn Leu Glu Glu	Leu Ser Arg Leu Thr	Gly Gly Leu Lys Phe	Phe
455	460		465
Val Pro Asp Ile	Ser Asn Ser Asn Ser	Met Ile Asp Ala Phe	Ser
470	475		480
Arg Ile Ser Ser	Gly Thr Gly Asp Ile	Phe Gln Gln His Ile	Gln
485	490		495
Leu Glu Ser Thr	Gly Glu Asn Val Lys	Pro His His Gln Leu	Lys
500	505		510
Asn Thr Val Thr	Val Asp Asn Thr Val	Gly Asn Asp Thr Met	Phe
515	520		525
Leu Val Thr Trp	Gln Ala Ser Gly Pro	Pro Glu Ile Ile Leu	Phe
530	535		540
Asp Pro Asp Gly	Arg Lys Tyr Tyr Thr	Asn Asn Phe Ile Thr	Asn
545	550		555
Leu Thr Phe Arg	Thr Ala Ser Leu Trp	Ile Pro Gly Thr Ala	Lys
560	565		570
Pro Gly His Trp	Thr Tyr Thr Leu Asn	Asn Thr His His Ser	Leu
575	580		585
Gln Ala Leu Lys	Val Thr Val Thr Ser	Arg Ala Ser Asn Ser	Ala
590	595		600
Val Pro Pro Ala	Thr Val Glu Ala Phe	Val Glu Arg Asp Ser	Leu
605	610		615
His Phe Pro His	Pro Val Met Ile Tyr	Ala Asn Val Lys Gln	Gly
620	625		630
Phe Tyr Pro Ile	Leu Asn Ala Thr Val	Thr Ala Thr Val Glu	Pro
635	640		645
Glu Thr Gly Asp	Pro Val Thr Leu Arg	Leu Leu Asp Asp Gly	Ala
650	655		660
Gly Ala Asp Val	Ile Lys Asn Asp Gly	Ile Tyr Ser Arg Tyr	Phe
665	670		675
Phe Ser Phe Ala	Ala Asn Gly Arg Tyr	Ser Leu Lys Val His	Val
680	685		690
Asn His Ser Pro	Ser Ile Ser Thr Pro	Ala His Ser Ile Pro	Gly
695	700		705
Ser His Ala Met	Tyr Val Pro Gly Tyr	Thr Ala Asn Gly Asn	Ile
710	715		720
Gln Met Asn Ala	Pro Arg Lys Ser Val	Gly Arg Asn Glu Glu	Glu
725	730		735
Arg Lys Trp Gly	Phe Ser Arg Val Ser	Ser Gly Gly Ser Phe	Ser
740	745		750
Val Leu Gly Val	Pro Ala Gly Pro His	Pro Asp Val Phe Pro	Pro
755	760		765
Cys Lys Ile Ile	Asp Leu Glu Ala Val	Lys Val Glu Glu Glu	Leu
770	775		780
Thr Leu Ser Trp	Thr Ala Pro Gly Glu	Asp Phe Asp Gln Gly	Gln
785	790		795
Ala Thr Ser Tyr	Glu Ile Arg Met Ser	Lys Ser Leu Gln Asn	Ile
800	805		810
Gln Asp Asp Phe	Asn Asn Ala Ile Leu	Val Asn Thr Ser Lys	Arg
815	820		825
Asn Pro Gln Gln	Ala Gly Ile Arg Glu	Ile Phe Thr Phe Ser	Pro
830	835		840
Gln Ile Ser Thr	Asn Gly Pro Glu His	Gln Pro Asn Gly Glu	Thr
845	850		855

His	Glu	Ser	His	Arg	Ile	Tyr	Val	Ala	Ile	Arg	Ala	Met	Asp	Arg	
				860					865					870	
Asn	Ser	Leu	Gln	Ser	Ala	Val	Ser	Asn	Ile	Ala	Gln	Ala	Pro	Leu	
				875					880					885	
Phe	Ile	Pro	Pro	Asn	Ser	Asp	Pro	Val	Pro	Ala	Arg	Asp	Tyr	Leu	
				890					895					900	
Ile	Leu	Lys	Gly	Val	Leu	Thr	Ala	Met	Gly	Leu	Ile	Gly	Ile	Ile	
				905					910					915	
Cys	Leu	Ile	Ile	Val	Val	Thr	His	His	Thr	Leu	Ser	Arg	Lys	Lys	
				920					925					930	
Arg	Ala	Asp	Lys	Lys	Glu	Asn	Gly	Thr	Lys	Leu	Leu				
				935					940						

<210> 10

<211> 519

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3148427CD1

<400> 10

Met	Glu	Glu	Met	Phe	His	Lys	Lys	Ser	Glu	Ala	Val	Arg	Arg	Leu	
1				5					10					15	
Val	Glu	Ala	Ala	Glu	Glu	Ala	His	Leu	Lys	His	Glu	Phe	Asp	Ala	
				20					25					30	
Asp	Leu	Gln	Tyr	Gly	Tyr	Phe	Asn	Ala	Val	Leu	Ile	Asn	Glu	Arg	
				35					40					45	
Asp	Lys	Asp	Gly	Asn	Phe	Leu	Glu	Leu	Gly	Lys	Glu	Phe	Ile	Leu	
				50					55					60	
Ala	Pro	Asn	Asp	His	Phe	Asn	Asn	Leu	Pro	Val	Asn	Ile	Ser	Leu	
				65					70					75	
Ser	Asp	Val	Gln	Val	Pro	Thr	Asn	Met	Tyr	Asn	Lys	Asp	Pro	Ala	
				80					85					90	
Ile	Val	Asn	Gly	Val	Tyr	Trp	Ser	Glu	Ser	Leu	Asn	Lys	Val	Phe	
				95					100					105	
Val	Asp	Asn	Phe	Asp	Arg	Asp	Pro	Ser	Leu	Ile	Trp	Gln	Tyr	Phe	
				110					115					120	
Gly	Ser	Ala	Lys	Gly	Phe	Phe	Arg	Gln	Tyr	Pro	Gly	Ile	Lys	Trp	
				125					130					135	
Glu	Pro	Asp	Glu	Asn	Gly	Val	Ile	Ala	Phe	Asp	Cys	Arg	Asn	Arg	
				140					145					150	
Lys	Trp	Tyr	Ile	Gln	Ala	Ala	Thr	Ser	Pro	Lys	Asp	Val	Val	Ile	
				155					160					165	
Leu	Val	Asp	Val	Ser	Gly	Ser	Met	Lys	Gly	Leu	Arg	Leu	Thr	Ile	
				170					175					180	
Ala	Lys	Gln	Thr	Val	Ser	Ser	Ile	Leu	Asp	Thr	Leu	Gly	Asp	Asp	
				185					190					195	
Asp	Phe	Phe	Asn	Ile	Ile	Ala	Tyr	Asn	Glu	Glu	Leu	His	Tyr	Val	
				200					205					210	
Glu	Pro	Cys	Leu	Asn	Gly	Thr	Leu	Val	Gln	Ala	Asp	Arg	Thr	Asn	
				215					220					225	
Lys	Glu	His	Phe	Arg	Glu	His	Leu	Asp	Lys	Leu	Phe	Ala	Lys	Gly	
				230					235					240	

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Ile Gly Met Leu Asp Ile Ala Leu Asn Glu Ala Phe Asn Ile Leu
    245                      250                      255
Ser Asp Phe Asn His Thr Gly Gln Gly Ser Ile Cys Ser Gln Ala
    260                      265                      270
Ile Met Leu Ile Thr Asp Gly Ala Val Asp Thr Tyr Asp Thr Ile
    275                      280                      285
Phe Ala Lys Tyr Asn Trp Pro Asp Arg Lys Val Arg Ile Phe Thr
    290                      295                      300
Tyr Leu Ile Gly Arg Glu Ala Ala Phe Ala Asp Asn Leu Lys Trp
    305                      310                      315
Met Ala Cys Ala Asn Lys Gly Phe Phe Thr Gln Ile Ser Thr Leu
    320                      325                      330
Ala Asp Val Gln Glu Asn Val Met Glu Tyr Leu His Val Leu Ser
    335                      340                      345
Arg Pro Lys Val Ile Asp Gln Glu His Asp Val Val Trp Thr Glu
    350                      355                      360
Ala Tyr Ile Asp Ser Thr Leu Pro Gln Ala Gln Lys Leu Thr Asp
    365                      370                      375
Asp Gln Gly Pro Val Leu Met Thr Thr Val Ala Met Pro Val Phe
    380                      385                      390
Ser Lys Gln Asn Glu Thr Arg Ser Lys Gly Ile Leu Leu Gly Val
    395                      400                      405
Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys Thr Ile Pro
    410                      415                      420
Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile Thr Asn
    425                      430                      435
Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Leu Tyr Glu
    440                      445                      450
Glu Gly Lys Lys Arg Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu
    455                      460                      465
Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala
    470                      475                      480
Met Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys
    485                      490                      495
Thr Val Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Leu
    500                      505                      510
Asn Leu Lys Gln Thr Thr Val Lys Asn
    515

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<210> 11

<211> 251

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3342358CD1

<400> 11

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Met Thr Asp Ser Ala Thr Ala Asn Gly Asp Asp Arg Asp Pro Glu
    1                      5                      10                      15
Ile Glu Leu Phe Val Lys Ala Gly Ile Asp Gly Glu Ser Ile Gly
    20                      25                      30
Asn Cys Pro Phe Ser Gln Arg Leu Phe Met Ile Leu Trp Leu Lys
    35                      40                      45

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<210> 12
<211> 323
<212> PRT
<213> Homo sapiens
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<400> 12

15/43

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Cys Ile Ala Ala Ser Glu Phe Tyr Lys Thr Arg His Asn Ile Ile
      125      130      135
Leu Ser Ala Gly Ile Phe Phe Val Ser Ala Gly Leu Ser Asn Ile
      140      145      150
Ile Gly Ile Ile Val Tyr Ile Ser Ala Asn Ala Gly Asp Pro Ser
      155      160      165
Lys Ser Asp Ser Lys Lys Asn Ser Tyr Ser Tyr Gly Trp Ser Phe
      170      175      180
Tyr Phe Gly Ala Leu Ser Phe Ile Ile Ala Glu Met Val Gly Val
      185      190      195
Leu Ala Val His Met Phe Ile Asp Arg His Lys Gln Leu Arg Ala
      200      205      210
Thr Ala Arg Ala Thr Asp Tyr Leu Gln Ala Ser Ala Ile Thr Arg
      215      220      225
Ile Pro Ser Tyr Arg Tyr Arg Tyr Gln Arg Arg Ser Arg Ser Ser
      230      235      240
Ser Arg Ser Thr Glu Pro Ser His Ser Arg Asp Ala Ser Pro Val
      245      250      255
Gly Ile Lys Gly Phe Asn Thr Leu Pro Ser Thr Glu Ile Ser Met
      260      265      270
Tyr Thr Leu Ser Arg Asp Pro Leu Lys Ala Ala Thr Thr Pro Thr
      275      280      285
Ala Thr Tyr Asn Ser Asp Arg Asp Asn Ser Phe Leu Gln Val His
      290      295      300
Asn Cys Ile Gln Lys Glu Asn Lys Asp Ser Leu His Ser Asn Thr
      305      310      315
Ala Asn Arg Arg Thr Thr Pro Val
      320

```

<210> 13

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1817329CD1

<400> 13

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Met Asn Gln Gly Ser Gly Leu Asp Leu Leu Lys Ile Ser Tyr Gly
  1      5      10      15
Lys Gly Ala Arg Arg Lys Asn Arg Phe Lys Gly Ser Asp Gly Ser
      20      25      30
Thr Ser Ser Asp Thr Thr Ser Asn Ser Phe Val Arg Gln Val Arg
      35      40      45
Val Leu Ser Ser Trp Phe
      50

```

<210> 14

<211> 113

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3273307CD1

<400> 14

Met	Glu	Gln	Arg	Lys	Leu	Asn	Asp	Gln	Ala	Asn	Thr	Leu	Val	Asp
1				5					10					15
Leu	Ala	Lys	Thr	Gln	Asn	Ile	Met	Tyr	Asp	Met	Ile	Ser	Asp	Leu
				20					25					30
Asn	Glu	Arg	Ser	Glu	Asp	Phe	Glu	Lys	Arg	Ile	Val	Thr	Leu	Glu
				35					40					45
Thr	Lys	Leu	Glu	Thr	Leu	Ile	Gly	Ser	Ile	His	Ala	Leu	Pro	Gly
				50					55					60
Leu	Ile	Ser	Gln	Thr	Ile	Arg	Gln	Gln	Gln	Arg	Asp	Phe	Ile	Glu
				65					70					75
Ala	Gln	Met	Glu	Ser	Tyr	Asp	Lys	His	Val	Thr	Tyr	Asn	Ala	Glu
				80					85					90
Arg	Ser	Arg	Ser	Ser	Ser	Arg	Arg	Arg	Arg	Ser	Ser	Ser	Thr	Ala
				95					100					105
Pro	Pro	Thr	Ser	Ser	Glu	Ser	Ser							
				110										

<210> 15

<211> 215

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3824833CD1

<400> 15

Met	His	Arg	Asp	Ala	Trp	Leu	Pro	Arg	Pro	Ala	Phe	Ser	Leu	Thr
1				5					10					15
Gly	Leu	Ser	Leu	Phe	Phe	Ser	Leu	Val	Pro	Pro	Gly	Arg	Ser	Met
				20					25					30
Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp
				35					40					45
Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His
				50					55					60
Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys
				65					70					75
Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu
				80					85					90
Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro
				95					100					105
Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu
				110					115					120
Asp	Glu	Gly	Ile	Tyr	Asn	Cys	Tyr	Ile	Met	Asn	Pro	Pro	Asp	Arg
				125					130					135
His	Arg	Gly	His	Gly	Lys	Ile	His	Leu	Gln	Val	Leu	Met	Glu	Glu
				140					145					150
Pro	Pro	Glu	Arg	Asp	Ser	Thr	Val	Ala	Val	Ile	Val	Gly	Ala	Ser
				155					160					165
Val	Gly	Gly	Phe	Leu	Ala	Val	Val	Ile	Leu	Val	Leu	Met	Val	Val
				170					175					180

Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp
 185 190 195
 Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro
 200 205 210
 Asp Asp Gly Ala Lys
 215

<210> 16
 <211> 235
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2069907CD1

<400> 16
 Met Phe Ile Trp Thr Ser Gly Arg Thr Ser Ser Ser Tyr Arg His
 1 5 10 15
 Asp Glu Lys Arg Asn Ile Tyr Gln Lys Ile Arg Asp His Asp Leu
 20 25 30
 Leu Asp Lys Arg Lys Thr Val Thr Ala Leu Lys Ala Gly Glu Asp
 35 40 45
 Arg Ala Ile Leu Leu Gly Leu Ala Met Met Val Cys Ser Ile Met
 50 55 60
 Met Tyr Phe Leu Leu Gly Ile Thr Leu Leu Arg Ser Tyr Met Gln
 65 70 75
 Ser Val Trp Thr Glu Glu Ser Gln Cys Thr Leu Leu Asn Ala Ser
 80 85 90
 Ile Thr Glu Thr Phe Asn Cys Ser Phe Ser Cys Gly Pro Asp Cys
 95 100 105
 Trp Lys Leu Ser Gln Tyr Pro Cys Pro Gln Val Tyr Val Asn Leu
 110 115 120
 Thr Ser Ser Gly Glu Lys Leu Leu Leu Tyr His Thr Glu Glu Thr
 125 130 135
 Ile Lys Ile Asn Gln Lys Cys Ser Tyr Ile Pro Lys Cys Gly Lys
 140 145 150
 Asn Phe Glu Glu Ser Met Ser Leu Val Asn Val Val Met Glu Asn
 155 160 165
 Phe Arg Lys Tyr Gln His Phe Ser Cys Tyr Ser Asp Pro Glu Gly
 170 175 180
 Asn Gln Lys Ser Val Ile Leu Thr Lys Leu Tyr Ser Ser Asn Val
 185 190 195
 Leu Phe His Ser Leu Phe Trp Pro Thr Cys Met Met Ala Gly Gly
 200 205 210
 Val Ala Ile Val Ala Met Val Lys Leu Thr Gln Tyr Leu Ser Leu
 215 220 225
 Leu Cys Glu Arg Ile Gln Arg Ile Asn Arg
 230 235

<210> 17
 <211> 234
 <212> PRT
 <213> Homo sapiens

<400> 17

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<210> 18
<211> 301
<212> PRT
<213> Homo sapiens
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<400> 18

19/43

Ala Gly Ser Leu	Ala Val Thr Ile	Ala Ile Tyr Val	Gly Gly Asn
65	70	75	
Val Ser Gly Ala	His Leu Asn Pro	Ala Phe Ser Leu	Ala Met Cys
80	85	90	
Ile Val Gly Arg	Leu Pro Trp Val	Lys Leu Pro Ile	Tyr Ile Leu
95	100	105	
Val Gln Leu Leu	Ser Ala Phe Cys	Ala Ser Gly Ala	Thr Tyr Val
110	115	120	
Leu Tyr His Asp	Ala Leu Gln Asn	Tyr Thr Gly Gly	Asn Leu Thr
125	130	135	
Val Thr Gly Pro	Lys Glu Thr Ala	Ser Ile Phe Ala	Thr Tyr Pro
140	145	150	
Ala Pro Tyr Leu	Ser Leu Asn Asn	Gly Phe Leu Asp	Gln Val Leu
155	160	165	
Gly Thr Gly Met	Leu Ile Val Gly	Leu Leu Ala Ile	Leu Asp Arg
170	175	180	
Arg Asn Lys Gly	Val Pro Ala Gly	Leu Glu Pro Val	Val Val Gly
185	190	195	
Met Leu Ile Leu	Ala Leu Gly Leu	Ser Met Gly Ala	Asn Cys Gly
200	205	210	
Ile Pro Leu Asn	Pro Ala Arg Asp	Leu Gly Pro Arg	Leu Phe Thr
215	220	225	
Tyr Val Ala Gly	Trp Gly Pro Glu	Val Phe Ser Ala	Gly Asn Gly
230	235	240	
Trp Trp Trp Val	Pro Val Val Ala	Pro Leu Val Gly	Ala Thr Val
245	250	255	
Gly Thr Ala Thr	Tyr Gln Leu Leu	Val Ala Leu His	His Pro Glu
260	265	270	
Gly Pro Glu Pro	Ala Gln Asp Leu	Val Ser Ala Gln	His Lys Ala
275	280	285	
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<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1568324CB1

<400> 19

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<211> 1298

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 4094907CB1

<400> 20

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<210> 21

<211> 1877

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 518158CB1

<400> 21

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<211> 2517

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte ID No: 602926CB1

<400> 22

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<211> 1154

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 922119CB1

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<211> 1879

<212> DNA

<213> Homo sapiens

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<221> misc_feature

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<400> 24

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1879

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<211> 1537

<212> DNA

<213> Homo sapiens

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<400> 25

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1537

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 <213> Homo sapiens

<220>
 <221> unsure
 <222> 790, 827, 860
 <223> a or g or c or t, unknown, or other

<220>
 <221> misc_feature
 <223> Incyte ID No: 1375415CB1

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<210> 28

<211> 1774

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3148427CB1

<400> 28

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<210> 29

<211> 1505

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 3342358CB1

<400> 29

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<210> 30
 <211> 1478
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1267774CB1

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<210> 31
 <211> 1971
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1817329CB1

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<210> 32

<211> 1424

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3273307CB1

<400> 32

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<210> 33

<211> 1224

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3824833CB1

<400> 33

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cgcccgctg ccctgcacct tcaactcctg ctacacagtg aaccacaaac agttctccct 360
gaactggact taccaggagt gcaacaactg ctctgaggag atgttccctc agttccgcat 420
gaagatcatt aacctgaagc tggagcgggt tcaagaccgc gtggagttct cagggaaccc 480
cagcaagtac gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 540
caactgctac atcatgaacc cccctgaccg ccaccgtggg catggcaaga tccatctgca 600
ggtcctcatg gaagagcccc ctgagcggga ctccacggtg gccgtgattg tgggtgcctc 660
cgtcgggggc ttcttggtg tggtcatctt ggtgctgatg gtggtcaagt gtgtgaggag 720
aaaaaaagag cagaagctga gcacagatga cctgaagacc gaggaggagg gcaagacgga 780
cgggtgaagg aacccgatg atggcgccaa gtagtgggtg gccggcctgc agcctcctc 840
aggggttgca cccagcgtc cctcaggagg gccttggcct ggcacggctg tgctcctccc 900
ctgctcccag cccagagcag ccatcagggt ggaggtgacg atgagttcct gaaacttgga 960
ggggcatgtt aaagggatga ctgtgcattc cagggcactg acggaaagcc agggctgcag 1020
gcaaagctgg acatgtgccc tggcccagga ggccatgttg ggccctcgtt tccattgcta 1080
gtggcctcct tggggctcct gttggctcct aatcccttag gactgtggat gaggccagac 1140
tggaagagca gctccaggta gggggccatg tttcccagcg gggacccacc aacagaggcc 1200
agtttcaaag tcagctgagg ggct 1224

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<210> 34

<211> 1300

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2069907CB1

<400> 34

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caccttggtg taaatgctgc tgggcaccgt tctgttttct ttcttttctt aatcctatcc 120
aagtatgcag tacgctcttg ggtcgtctca tgagaccagc gggcatgttg gaaagaactg 180
agagaaaagag caacaaagcg gcgagtgggt tgagagggca gcacgcgctg tggggccctt 240
ccagagaaat gtactgaaaa agtctacgca atgtctggga tttgctaaac aatacctgga 300
aagcagacag gtctttttgc cattcctcca ggacatccac cataaggaaa ggagaccctg 360

```

```

gaccaacatt ctctaagatg tttatatgga ccagtggccg gacctcttca tcttatagac 420
atgatgaaaa aagaaatatt taccagaaaa tcagggacca tgacctcctg gacaaaagga 480
aaacagtcac agcactgaag gcaggagagg accgagctat tctcctggga ctggctatga 540
tggtgtgctc catcatgatg tatcttctgc tgggaatcac actcctgcgc tcatacatgc 600
agagcgtgtg gaccgaagag tctcaatgca ccttgctgaa tgcgtccatc acggaaacat 660
ttaactgctc cttcagctgt ggtccagact gctggaaact ttctcagtac ccctgcccc 720
aggtgtacgt taacctgact tcttccgggg aaaagctcct cctctaccac acagaagaga 780
caataaaaaat caatcagaag tgctcctata tacctaaatg tggaaaaaat tttgaagaat 840
ccatgtccct ggtgaatgtt gtcatggaaa acttcaggaa gtatcaacac ttctcctgct 900
attctgaccc agaaggaaac cagaagagtg ttatcctaac caaactctac agttccaacg 960
tgctgttcca ttcactcttc tggccaacct gtatgatggc tgggggtgtg gcaattgttg 1020
ccatggtgaa acttacacag tacctctccc tactatgtga gaggatccaa cggatcaata 1080
gataaatgca aaaatggata aaataatttt tgtaaagct caaataactgt tttctttcat 1140
tcttcaccaa agaaccttaa gtttgtaacg tgcagtctgt tatgagttcc ctaatatatt 1200
cttatatgta gagcaataat gcaaaaagctg ttctatatgc aaacatgatg tctttattat 1260
tcaggagaaat aaataactgt tttgtgttaa aaaaaaaaaa 1300

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<210> 35

<211> 1060

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2243917CB1

<400> 35

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gcttgctggg atcatggcgg agaatcactg cgagctcctg tcgccggccc ggggcggcat 60
cggggcgggg ctggggggcg gcctgtgccg ccgctgcagc gctgggctcg gcgccctggc 120
ccagcgccct ggcagcgtgt ccaagtgggt ccgactcaac gtcggcgga cctacttct 180
caccactcgg cagacctgt gccgggaccc gaaatccttc ctgtaccgt tatgccaggc 240
cgatccccgac ctggactcag acaaggatga aacaggcgcc tatttaatcg acagagaccc 300
cacctacttt gggcctgtgc tgaactacct gagacacggc aagctggtga ttaacaaaga 360
cctcgcggag gaaggagtgt tggaggaagc agaattttac aatatcacct cattaataaa 420
acttgtaaag gacaaaatta gagaacgaga cagcaaaaca tcgcaggtgc ctgtgaagca 480
tgtgtaccgt gtgctgcagt gccaggagga ggagctcacg cagatggtgt ccaccatgtc 540
cgacggctcg aagttcgagc agttggtcag catcggtcc tcttacaact atgggaacga 600
agaccaagcc gagttcctct gtgtggtgtc caaggagctg cacaacaccc cgtacggtac 660
ggccagcgag cccagcgaga aggccaagat tttgcaagaa cgaggctcaa ggatgtgagg 720
gacacagtat tgacagctga agaaatgatt tacgttttcc cgagatgtaa tgaactgcca 780
tgtccaggaa gcttggtgtg gagaagaaac ctgcttttga tcatttttct agagatctgg 840
gtgtgaatec tttttgcct ctgaggtggg tgggtgagaga cgggcccagc tgtccaaggc 900
cagacgtccc caagttgggg gagcacggcg gccgggtggg cgctgcctct tggggggggc 960
tcgctctgtt ttttccaagt gccacgtggg actgaggcag acactcccag tcagcccgtc 1020
cgatcctgaa gatcgtgtga aggaagcgtt cttggtgcta 1060

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<210> 36

<211> 1815

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2597476CB1

<400> 36

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gtgcctatgc agacagaggg agcagtgaat agcaataggg tgtttccacc atgggtcttca 60
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gcctggcaga gtttctgggt gtgtttgtac tcatgctcct cacccaagga gctgtggccc 180
aggctgtcac cagtggagaa accaaaggca acttcttcac catgtttctg gctggtcttc 240
tggecggtac gatagccatc tacgtgggtg gtaacgtctc aggggcccac ctgaatccag 300
ccttctccct ggccatgtgc atcgttggac gcctcccctg ggtcaagctc cccatttaca 360
tcttgggtgca gttgctgtct gctttctgtg cttcgggagc cacctatgtt ctctaccatg 420
atgccctaca gaactataca ggtgggaacc tgacagtgc tggtcccaag gagacagcct 480
ccatttttgc cacctatcct gccccctatc tgtccctgaa caatggcttc ctggatcagg 540
ttctgggcac tgggatgctg attgtggggc tcttggccat cctggacaga cggaacaagg 600
gagtcctctg gggctctggag cctgtgggtg tggggatgct gatcctggcc ctcggttat 660
ccatgggtgc caactgcggg attccactca accctgcccg ggacctgggc ccacgtctct 720
tcacctacgt ggctggctgg ggtcctgaag tcttcagtgc tggtaatggc tgggtggtgg 780
tgcctgtggt gggccctctg gtgggggcca ccgttggcac agccacttac cagctgttgg 840
tggctctgca ccacctgag gggccagagc cagctcagga tctggtgtct gctcaacaca 900
aagcctcaga gttggaaact cctgcctcag ctcagatgct ggagtgtgaa ctatgattag 960
gacaaccctc acttactca tggaccctgg agccagccac tgaccccgcc tgggaacaac 1020
agtcattctt cctctttgtt aatgtgccag aacctgggag gcttctctgt ttatctgttt 1080
ggcatccctt cctcctaaac taagaaggat cctggacagg gagaagtgga ggaggataag 1140
gtaccaggac tcaggcttct catccctcc tcccgcaaag cggttttctg accctcaggg 1200
cctctcgga tgtagtgtc cgaggtaacc gctagagggt gcgcacctgg atgctggatg 1260
gggacggctg cgggcatctg cagggtggag gggggccacca tccagtgtag ggcacaaccc 1320
tggggactgc cctccatagc ctgtcccgac tgccgactcc tagctctcat cgcctcggcg 1380
cctccacct tcacctctc ggggatgcct cccaagagg gtagttaggg gtggggaagc 1440
cgctccacc cagggggcgt ggtgggggcg gagggaagga gggcgggcgg gcacagagac 1500
agagagcaag gctgtgaaac tgaggcaccg ttcctagaca tctcggtgct gtgtcgttca 1560
ttcaaggaga gttgagatac agtgaaatga gccagggcga ggaggaggag tgaaggaacg 1620
gagggcgggc ggctccgagg agcgagagtc gggctgaggg caacctggcg ccagggaaaa 1680
ttctggttat tcaccacttc tacagctctc ctgccgctcc ctgcagagga tgctcgtttt 1740
gcagagaagg cagtgttctt ctattccctt cttccgaatt aaaaataccc cctcagagcg 1800
aaaaaaaaaa aaaaaa 1815

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<210> 37

<211> 315

<212> PRT

<213> Rattus norvegicus

<220>

<221> misc_feature

<223> GenBank ID No: g2924369

<400> 37

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Met Leu Gly Trp Val Gln Arg Val Leu Pro Gln Pro Pro Gly Thr
 1          5          10          15
Pro Gln Lys Thr Glu Gly Ala Gly Pro Gln Pro Glu Thr Glu
 20          25          30
Ser Lys Pro Glu Ala Asn Pro Gln Pro Glu Pro Glu Val Gln Pro
 35          40          45
Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Ala
 50          55          60
Pro Glu Glu Ala Ala Pro Glu Val Gln Thr Leu Pro Pro Glu Glu
 65          70          75
Pro Val Glu Gly Glu Asp Val Ala Glu Ala Gly Pro Ser Leu Gln
 80          85          90
Glu Thr Gln Glu Ala Asp Pro Pro Gln Pro Thr Ser Gln Ala Gln
 95          100         105

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Val	Ala	Val	Val	Lys	Val	Asn	Arg	Pro	Ser	Ser	Trp	Met	Leu	Ser
				110					115					120
Trp	Phe	Trp	Lys	Gly	Met	Glu	Lys	Val	Val	Pro	Gln	Pro	Val	Tyr
				125					130					135
Ser	Ser	Ser	Gly	Gly	Gln	Asn	Leu	Ala	Ala	Gly	Glu	Gly	Gly	Pro
				140					145					150
Asp	Gln	Asp	Gly	Ala	Gln	Thr	Leu	Glu	Pro	Cys	Gly	Thr	Gly	Asp
				155					160					165
Pro	Gly	Ser	Glu	Asp	Gly	Ser	Asp	Lys	Thr	Ser	Lys	Thr	Gln	Asp
				170					175					180
Thr	Glu	Pro	Ser	Leu	Trp	Leu	Leu	Arg	Trp	Leu	Glu	Leu	Asn	Leu
				185					190					195
Glu	Lys	Val	Leu	Pro	Gln	Pro	Pro	Thr	Pro	Ser	Gln	Ala	Trp	Lys
				200					205					210
Val	Glu	Pro	Glu	Gly	Ala	Val	Leu	Glu	Pro	Asp	Pro	Pro	Gly	Thr
				215					220					225
Pro	Met	Glu	Val	Glu	Pro	Thr	Glu	Asn	Pro	Ser	Gln	Pro	Asn	Pro
				230					235					240
Gly	Pro	Val	Glu	Pro	Glu	Glu	Glu	Pro	Ala	Ala	Glu	Pro	Gln	Pro
				245					250					255
Gly	Phe	Gln	Ala	Ser	Ser	Leu	Pro	Pro	Pro	Gly	Asp	Pro	Val	Arg
				260					265					270
Leu	Ile	Glu	Trp	Leu	Leu	His	Arg	Leu	Glu	Met	Ala	Leu	Pro	Gln
				275					280					285
Pro	Val	Leu	His	Gly	Lys	Ala	Ala	Glu	Gln	Glu	Pro	Ser	Cys	Pro
				290					295					300
Gly	Thr	Cys	Asp	Val	Gln	Thr	Arg	Ala	Thr	Ala	Ala	Gly	Gly	Leu
				305					310					315

<210> 38

<211> 490

<212> PRT

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<223> GenBank ID No: g116443

<400> 38

Met	Ala	Ser	Val	Ala	Ala	Trp	Leu	Pro	Phe	Ala	Arg	Ala	Ala	Ala
1				5					10					15
Ile	Gly	Trp	Val	Pro	Ile	Ala	Thr	His	Pro	Leu	Pro	Pro	Pro	Pro
				20					25					30
Met	Pro	Lys	Asp	Arg	Arg	Lys	Thr	Asp	Asp	Glu	Lys	Leu	Leu	Ile
				35					40					45
Asn	Val	Ser	Gly	Arg	Arg	Phe	Glu	Thr	Trp	Arg	Asn	Thr	Leu	Glu
				50					55					60
Lys	Tyr	Pro	Asp	Thr	Leu	Leu	Gly	Ser	Asn	Glu	Arg	Glu	Phe	Phe
				65					70					75
Tyr	Asp	Glu	Asp	Cys	Lys	Glu	Tyr	Phe	Phe	Asp	Arg	Asp	Pro	Asp
				80					85					90
Ile	Phe	Arg	His	Ile	Leu	Asn	Tyr	Tyr	Arg	Thr	Gly	Lys	Leu	His
				95					100					105
Tyr	Pr	Lys	His	Glu	Cys	Leu	Thr	Ser	Tyr	Asp	Glu	Glu	Leu	Ala
				110					115					120

Phe	Phe	Gly	Ile	Met	Pro	Asp	Val	Ile	Gly	Asp	Cys	Cys	Tyr	Glu
				125										135
Asp	Tyr	Arg	Asp	Arg	Lys	Arg	Glu	Asn	Ala	Glu	Arg	Leu	Met	Asp
				140										150
Asp	Lys	Leu	Ser	Glu	Asn	Gly	Asp	Gln	Asn	Leu	Gln	Gln	Leu	Thr
				155										165
Asn	Met	Arg	Gln	Lys	Met	Trp	Arg	Ala	Phe	Glu	Asn	Pro	His	Thr
				170										180
Ser	Thr	Ser	Ala	Leu	Val	Phe	Tyr	Tyr	Val	Thr	Gly	Phe	Phe	Ile
				185										195
Ala	Val	Ser	Val	Met	Ala	Asn	Val	Val	Glu	Thr	Val	Pro	Cys	Gly
				200										210
His	Arg	Pro	Gly	Arg	Ala	Gly	Thr	Leu	Pro	Cys	Gly	Glu	Arg	Tyr
				215										225
Lys	Ile	Val	Phe	Phe	Cys	Leu	Asp	Thr	Ala	Cys	Val	Met	Ile	Phe
				230										240
Thr	Ala	Glu	Tyr	Leu	Leu	Arg	Leu	Phe	Ala	Ala	Pro	Asp	Arg	Cys
				245										255
Lys	Phe	Val	Arg	Ser	Val	Met	Ser	Ile	Ile	Asp	Val	Val	Ala	Ile
				260										270
Met	Pro	Tyr	Tyr	Ile	Gly	Leu	Gly	Ile	Thr	Asp	Asn	Asp	Asp	Val
				275										285
Ser	Gly	Ala	Phe	Val	Thr	Leu	Arg	Val	Phe	Arg	Val	Phe	Arg	Ile
				290										300
Phe	Lys	Phe	Ser	Arg	His	Ser	Gln	Gly	Leu	Arg	Ile	Leu	Gly	Tyr
				305										315
Thr	Leu	Lys	Ser	Cys	Ala	Ser	Glu	Leu	Gly	Phe	Leu	Val	Phe	Ser
				320										330
Leu	Ala	Met	Ala	Ile	Ile	Ile	Phe	Ala	Thr	Val	Met	Phe	Tyr	Ala
				335										345
Glu	Lys	Asn	Val	Asn	Gly	Thr	Asn	Phe	Thr	Ser	Ile	Pro	Ala	Ala
				350										360
Phe	Trp	Tyr	Thr	Ile	Val	Thr	Met	Thr	Thr	Leu	Gly	Tyr	Gly	Asp
				365										375
Met	Val	Pro	Glu	Thr	Ile	Ala	Gly	Lys	Ile	Val	Gly	Gly	Val	Cys
				380										390
Ser	Leu	Ser	Gly	Val	Leu	Val	Ile	Ala	Leu	Pro	Val	Pro	Val	Ile
				395										405
Val	Ser	Asn	Phe	Ser	Arg	Ile	Tyr	His	Gln	Asn	Gln	Arg	Ala	Asp
				410										420
Lys	Arg	Lys	Ala	Gln	Arg	Lys	Ala	Arg	Leu	Ala	Arg	Ile	Arg	Ile
				425										435
Ala	Lys	Ala	Ser	Ser	Gly	Ala	Ala	Phe	Val	Ser	Lys	Lys	Lys	Ala
				440										450
Ala	Glu	Ala	Arg	Trp	Ala	Ala	Gln	Glu	Ser	Gly	Ile	Glu	Leu	Asp
				455										465
Asp	Asn	Tyr	Arg	Asp	Glu	Asp	Ile	Phe	Glu	Leu	Gln	His	His	His
				470										480
Leu	Leu	Arg	Cys	Leu	Glu	Lys	Thr	Thr	Met					
				485										490

<210> 39

<211> 478

<212> PRT

<213> Polyorchis penicillatus

<220>

<221> misc_feature

<223> GenBank ID No: g1763619

<400> 39

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Met Asn Gly Asp Ile Gly Ala Trp Ile Ser Cys Ala Arg Thr Ala
 1          5          10          15
Gly Ile Gly Trp Val Pro Ile Ser Ser Lys Glu Pro Ser Ala Tyr
          20          25          30
Leu Asn Lys Gln Val Cys Asn Glu Asn Glu Lys Asn Asn Ala Lys
          35          40          45
Leu Thr Ile Asn Val Ser Gly Arg Arg Tyr Gln Thr Tyr Ser His
          50          55          60
Thr Leu Arg Lys Phe Lys Glu Thr Leu Leu Gly Ser Gln Glu Arg
          65          70          75
Asp Tyr Phe Tyr Asp Glu Ser Leu Glu Glu Tyr Tyr Phe Asp Arg
          80          85          90
Asp Pro Asp Leu Phe Arg His Ile Leu Asn Tyr Tyr Arg Thr Gly
          95          100          105
Lys Leu His Phe Pro Lys Asn Glu Cys Val Ser Ser Phe Glu Asp
          110          115          120
Glu Leu Thr Phe Phe Gly Ile Lys Gly Phe Asn Ile Asn Asn Cys
          125          130          135
Cys Trp Asp Asp Tyr His Asp Lys Lys Arg Glu Cys Thr Glu Arg
          140          145          150
Leu Asn Glu Ser Asp Val Met Leu Thr Ser Ser Glu Ile Asn Glu
          155          160          165
Lys Ser Asp Thr Met Gly Ile Asp Val Gln Met Asn Asn His Gln
          170          175          180
Ala Lys Asn Phe Arg Gln Lys Val His Gly Leu Phe Glu Asn Pro
          185          190          195
Gln Ser Thr Phe Leu Ala Arg Ile Leu Tyr Tyr Ile Thr Gly Phe
          200          205          210
Phe Ile Ala Val Ser Val Gly Ser Thr Ile Ile Glu Thr Ile Asp
          215          220          225
Cys Ser Ala Asn Arg Pro Cys Gly Glu Val Tyr Asn Lys Ile Phe
          230          235          240
Phe Asn Ile Glu Ala Val Cys Val Val Val Phe Thr Ile Glu Tyr
          245          250          255
Leu Ala Arg Leu Tyr Ser Ala Pro Cys Arg Phe Arg His Ala Arg
          260          265          270
Ile Ser Leu Ser Ile Ile Asp Val Ile Ala Ile Leu Pro Phe Tyr
          275          280          285
Ile Gly Leu Ala Met Thr Lys Thr Ser Ile Ser Gly Ala Phe Val
          290          295          300
Ser Leu Arg Val Phe Arg Val Phe Arg Ile Phe Lys Phe Ser Arg
          305          310          315
His Ser Lys Gly Leu Arg Ile Leu Gly Ser Thr Leu Thr Ser Cys
          320          325          330
Ala Ser Glu Leu Gly Phe Leu Leu Phe Ser Leu Ser Met Ala Ile
          335          340          345
Ile Ile Phe Ala Thr Val Val Phe Tyr Val Glu Lys Asp Val Asn
          350          355          360
Asp Ser Asp Phe Thr Ser Ile Pro Ala Ser Phe Trp Tyr Thr Ile
          365          370          375
Val Thr Met Thr Thr Leu Gly Tyr Gly Asp Met Val Pro Lys Thr

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	380		385		390
Ile Pro Gly Lys	Leu Val Gly Ser Ile	Cys Ser Leu Ser Gly Val			
	395	400		405	
Leu Val Ile Ala	Leu Pro Val Pro Val	Ile Val Ser Asn Phe Ser			
	410	415		420	
Arg Ile Tyr Leu	Gln Asn Gln Arg Ala	Asp Lys Arg Arg Ala Asn			
	425	430		435	
Gln Lys Leu Arg	Asn Lys Cys Glu Glu	Lys Glu Glu Lys Lys Lys			
	440	445		450	
Glu Ser Ser Ser	Glu Thr Val Thr Arg	Phe Ile Ile Ser Asn Gln			
	455	460		465	
Met Tyr Thr Ile	Phe Ser Met Lys Phe	Ala Leu Thr Arg			
	470	475			

<210> 40

<211> 732

<212> PRT

<213> Rattus norvegicus

<220>

<221> misc_feature

<223> GenBank ID No: g2564072

<400> 40

Met Asp Thr Ser Gly His Phe His Glu Ser Gly Val Gly Asp Leu		
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Asp Glu Asp Pro Lys Cys Pro Cys Pro Ser Ser Gly Asp Glu Gln		
	20	25
Gln Gln Gln Gln Gln Pro Pro Pro Pro Ser Ala Pro Pro Ala Val		
	35	40
Pro Gln Gln Pro Pro Gly Pro Leu Leu Gln Pro Gln Pro Pro Gln		
	50	55
Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln		
	65	70
Gln Gln Gln Gln Gln Ala Pro Leu His Pro Leu Pro Gln Leu Ala		
	80	85
Gln Leu Gln Ser Gln Val Val His Pro Gly Leu Leu His Ser Ser		
	95	100
Pro Thr Ala Phe Arg Ala Pro Asn Ser Ala Asn Ser Thr Ala Ile		
	110	115
Leu His Pro Ser Ser Arg Gln Gly Ser Gln Leu Asn Leu Asn Asp		
	125	130
His Leu Val Gly His Ser Pro Ser Ser Thr Ala Thr Ser Gly Pro		
	140	145
Gly Gly Gly Ser Arg His Arg Gln Ala Ser Pro Val Val His Arg		
	155	160
Arg Asp Ser Asn Pro Phe Thr Glu Ile Ala Met Ser Ser Cys Lys		
	170	175
Tyr Ser Gly Gly Val Met Lys Pro Leu Asn Arg Leu Ser Ala Ser		
	185	190
Arg Arg Asn Leu Ile Glu Ala Glu Pro Glu Gly Gln Pro Leu Gln		
	200	205
Leu Phe Ser Pro Ser Asn Pro Pro Glu Ile Ile Ile Ser Ser Arg		
	215	220
Glu Asp Asn His Ala His Gln Thr Leu Leu His His Pro Asn Ala		

	230		235		240
Thr His Asn His	Gln His Ala Gly Thr	Thr Ala Gly Ser Thr Thr			
	245		250		255
Phe Pro Lys Ala	Asn Lys Arg Lys Asn	Gln Asn Ile Gly Tyr Lys			
	260		265		270
Leu Gly His Arg	Arg Ala Leu Phe Glu	Lys Arg Lys Arg Leu Ser			
	275		280		285
Asp Tyr Ala Leu	Ile Phe Gly Met Phe	Gly Ile Val Val Met Val			
	290		295		300
Ile Glu Thr Glu	Leu Ser Trp Gly Leu	Tyr Ser Lys Asp Ser Met			
	305		310		315
Phe Ser Leu Ala	Leu Lys Cys Leu Ile	Ser Leu Ser Thr Ile Ile			
	320		325		330
Leu Leu Gly Leu	Ile Ile Ala Tyr His	Thr Arg Glu Val Gln Leu			
	335		340		345
Phe Val Ile Asp	Asn Gly Ala Asp Asp	Trp Arg Ile Ala Met Thr			
	350		355		360
Tyr Glu Arg Ile	Leu Tyr Ile Ser Leu	Glu Met Leu Val Cys Ala			
	365		370		375
Ile His Pro Ile	Pro Gly Glu Tyr Lys	Phe Phe Trp Thr Ala Arg			
	380		385		390
Leu Ala Phe Ser	Tyr Thr Pro Ser Arg	Ala Glu Ala Asp Val Asp			
	395		400		405
Ile Ile Leu Ser	Ile Pro Met Phe Leu	Arg Leu Tyr Leu Ile Ala			
	410		415		420
Arg Val Met Leu	Leu His Ser Lys Leu	Phe Thr Asp Ala Ser Ser			
	425		430		435
Arg Ser Ile Gly	Ala Leu Asn Lys Ile	Asn Phe Asn Thr Arg Phe			
	440		445		450
Val Met Lys Thr	Leu Met Thr Ile Cys	Pro Gly Thr Val Leu Leu			
	455		460		465
Val Phe Ser Ile	Ser Leu Trp Ile Ile	Ala Ala Trp Thr Val Arg			
	470		475		480
Val Cys Glu Arg	Tyr His Asp Gln Gln	Asp Val Thr Ser Asn Phe			
	485		490		495
Leu Gly Ala Met	Trp Leu Ile Ser Ile	Thr Phe Leu Ser Ile Gly			
	500		505		510
Tyr Gly Asp Met	Val Pro His Thr Tyr	Cys Gly Lys Gly Val Cys			
	515		520		525
Leu Leu Thr Gly	Ile Met Gly Ala Gly	Cys Thr Ala Leu Val Val			
	530		535		540
Ala Val Val Ala	Arg Lys Leu Glu Leu	Thr Lys Ala Glu Lys His			
	545		550		555
Val His Asn Phe	Met Met Asp Thr Gln	Leu Thr Lys Arg Ile Lys			
	560		565		570
Asn Ala Ala Ala	Asn Val Leu Arg Glu	Thr Trp Leu Ile Tyr Lys			
	575		580		585
His Thr Lys Leu	Leu Lys Lys Ile Asp	His Ala Lys Val Arg Lys			
	590		595		600
His Gln Arg Lys	Phe Leu Gln Ala Ile	His Gln Leu Arg Gly Val			
	605		610		615
Lys Met Glu Gln	Arg Lys Leu Ser Asp	Gln Ala Asn Thr Leu Val			
	620		625		630
Asp Leu Ser Lys	Met Gln Asn Val Met	Tyr Asp Leu Ile Thr Glu			
	635		640		645
Leu Asn Asp Arg	Ser Glu Asp Leu Glu	Lys Gln Ile Gly Ser Leu			

	650		655		660
Glu Ser Lys Leu	Glu His Leu Thr Ala	Ser Phe Asn Ser Leu Pro			
	665		670		675
Leu Leu Ile Ala	Asp Thr Leu Arg Gln	Gln Gln Gln Gln Leu Leu			
	680		685		690
Thr Ala Phe Val	Glu Ala Arg Gly Ile	Ser Val Ala Val Gly Thr			
	695		700		705
Ser His Ala Pro	Pro Ser Asp Ser Pro	Ile Gly Ile Ser Ser Thr			
	710		715		720
Ser Phe Pro Thr	Pro Tyr Thr Ser Ser	Ser Ser Cys			
	725		730		

<210> 41

<211> 269

<212> PRT

<213> Rattus norvegicus

<220>

<221> misc_feature

<223> GenBank ID No: g2350843

<400> 41

Met Ala Gly Ser Val	Leu Glu Asn Ile	Gln Ser Val Leu Gln Lys
1	5	10 15
Thr Trp Val Arg	Glu Phe Leu Ala Glu Phe	Leu Asn Thr Tyr Val
	20	25 30
Leu Met Val Phe	Gly Leu Gly Ser Val Ala	His Met Val Leu Gly
	35	40 45
Glu Arg Leu Gly	Ser Tyr Leu Gly Val Asn	Leu Gly Phe Gly Phe
	50	55 60
Gly Val Thr Met	Gly Ile His Val Ala Gly	Gly Ile Ser Gly Ala
	65	70 75
His Met Asn Pro	Ala Val Thr Phe Thr Asn	Cys Ala Leu Gly Arg
	80	85 90
Met Ala Gly Arg	Lys Phe Pro Ile Tyr Val	Leu Gly Gln Phe Leu
	95	100 105
Gly Ser Phe Leu	Ala Ala Ala Thr Thr Tyr	Leu Ile Phe Tyr Gly
	110	115 120
Ala Ile Asn His	Tyr Ala Gly Glu Thr Leu	Leu Val Thr Gly Pro
	125	130 135
Lys Ser Thr Ala	Asn Ile Phe Ala Thr Tyr	Leu Pro Glu His Met
	140	145 150
Thr Leu Trp Arg	Gly Phe Val Asp Glu Val	Phe Val Thr Gly Met
	155	160 165
Leu Gln Leu Cys	Ile Phe Ala Ile Thr Asp	Lys Leu Asn Ser Pro
	170	175 180
Ala Leu Gln Gly	Thr Glu Pro Leu Met Ile	Gly Ile Leu Val Cys
	185	190 195
Val Leu Gly Val	Ser Leu Gly Met Asn Thr	Gly Tyr Ala Ile Asn
	200	205 210
Pro Ser Arg Asp	Leu Pro Pro Arg Phe Phe	Thr Phe Ile Ala Gly
	215	220 225
Trp Gly Lys Lys	Val Phe Ser Ala Gly Asn	Asn Trp Trp Trp Val
	230	235 240
Pro Val Val Ala	Pro Leu Leu Gly Ala Tyr	Leu Gly Gly Ile Val

	245		250		255
Tyr	Leu	Gly	Leu	Ile	His
			Ala	Gly	Ile
			Pro	Pro	Gln
				Gly	Ser
	260		265		

<210> 42
 <211> 266
 <212> PRT
 <213> Mus musculus

<220>
 <221> misc_feature
 <223> GenBank ID No: g192647

<400> 42

Met	Asn	Trp	Gly	Phe	Leu	Gln	Gly	Ile	Leu	Ser	Gly	Val	Asn	Lys
1				5					10					15
Tyr	Ser	Thr	Ala	Leu	Gly	Arg	Ile	Trp	Leu	Ser	Val	Val	Phe	Ile
			20						25					30
Phe	Arg	Val	Leu	Val	Tyr	Val	Val	Ala	Ala	Glu	Glu	Val	Trp	Asp
			35						40					45
Asp	Asp	Gln	Lys	Asp	Phe	Ile	Cys	Asn	Thr	Lys	Gln	Pro	Gly	Cys
			50						55					60
Pro	Asn	Val	Cys	Tyr	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg
			65						70					75
Leu	Trp	Ala	Leu	Gln	Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu
			80						85					90
Val	Val	Met	His	Val	Ala	Tyr	Arg	Glu	Glu	Arg	Glu	Arg	Lys	His
			95						100					105
Arg	Leu	Lys	His	Gly	Pro	Asn	Ala	Pro	Ala	Leu	Tyr	Ser	Asn	Leu
			110						115					120
Ser	Lys	Lys	Arg	Gly	Gly	Leu	Trp	Trp	Thr	Tyr	Leu	Leu	Ser	Leu
			125						130					135
Ile	Phe	Lys	Ala	Ala	Val	Asp	Ser	Gly	Phe	Leu	Tyr	Ile	Phe	His
			140						145					150
Cys	Ile	Tyr	Lys	Asp	Tyr	Asp	Met	Pro	Arg	Val	Val	Ala	Cys	Ser
			155						160					165
Val	Thr	Pro	Cys	Pro	His	Thr	Val	Asp	Cys	Tyr	Ile	Ala	Arg	Pro
			170						175					180
Thr	Glu	Lys	Lys	Val	Phe	Thr	Tyr	Phe	Met	Val	Val	Thr	Ala	Ala
			185						190					195
Ile	Cys	Ile	Leu	Leu	Asn	Leu	Ser	Glu	Val	Val	Tyr	Leu	Val	Gly
			200						205					210
Lys	Arg	Cys	Met	Glu	Val	Phe	Arg	Pro	Arg	Arg	Arg	Lys	Ala	Ser
			215						220					225
Arg	Arg	His	Gln	Leu	Pro	Asp	Thr	Cys	Pro	Pro	Tyr	Val	Ile	Ser
			230						235					240
Lys	Gly	Gly	His	Pro	Gln	Asp	Glu	Ser	Val	Ile	Leu	Thr	Lys	Ala
			245						250					255
Gly	Met	Ala	Thr	Val	Asp	Ala	Gly	Val	Tyr	Pro				
			260						265					

<210> 43
 <211> 191
 <212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> GenBank ID No: g1055345

<400> 43

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Met Val Lys Lys Leu Val Met Ala Gln Lys Arg Gly Glu Thr Arg
 1              5              10              15
Ala Leu Cys Leu Gly Val Thr Met Val Val Cys Ala Val Ile Thr
      20              25              30
Tyr Tyr Ile Leu Val Thr Thr Val Leu Pro Leu Tyr Gln Lys Ser
      35              40              45
Val Trp Thr Gln Glu Ser Lys Cys His Leu Ile Glu Thr Asn Ile
      50              55              60
Arg Asp Gln Glu Glu Leu Lys Gly Lys Lys Val Pro Gln Tyr Pro
      65              70              75
Cys Leu Trp Val Asn Val Ser Ala Ala Gly Arg Trp Ala Val Leu
      80              85              90
Tyr His Thr Glu Asp Thr Arg Asp Gln Asn Gln Gln Cys Ser Tyr
      95              100             105
Ile Pro Gly Ser Val Asp Asn Tyr Gln Thr Ala Arg Ala Asp Val
      110             115             120
Glu Lys Val Arg Ala Lys Phe Gln Glu Gln Gln Val Phe Tyr Cys
      125             130             135
Phe Ser Ala Pro Arg Gly Asn Glu Thr Ser Val Leu Phe Gln Arg
      140             145             150
Leu Tyr Gly Pro Gln Ala Leu Leu Phe Ser Leu Phe Trp Pro Thr
      155             160             165
Phe Leu Leu Thr Gly Gly Leu Leu Ile Ile Ala Met Val Lys Ser
      170             175             180
Asn Gln Tyr Leu Ser Ile Leu Ala Ala Gln Lys
      185             190

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<210> 44

<211> 308

<212> PRT

<213> Caenorhabditis elegans

<220>

<221> misc_feature

<223> GenBank ID No: g3292929

<400> 44

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Met Ser Thr Val Phe Ile Asn Ser Arg Lys Ser Pro Asn Val Leu
 1              5              10              15
Lys Lys Gln Gly Thr Asp Gln Trp Val Lys Leu Asn Val Gly Gly
      20              25              30
Thr Tyr Phe Leu Thr Thr Lys Thr Thr Leu Ser Arg Asp Pro Asn
      35              40              45
Ser Phe Leu Ser Arg Leu Ile Gln Glu Asp Cys Asp Leu Ile Ser
      50              55              60
Asp Arg Asp Glu Thr Gly Ala Tyr Leu Ile Asp Arg Asp Pro Lys
      65              70              75
Tyr Phe Ala Pro Val Leu Asn Tyr Leu Arg His Gly Lys Leu Val

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	80		85		90
Leu Asp Gly Val	Ser Glu Glu Gly Val	Leu Glu Glu Ala Glu Phe			
	95		100		105
Tyr Asn Val Thr	Gln Leu Ile Ala Leu	Leu Lys Glu Cys Ile Leu			
	110		115		120
His Arg Asp Gln	Arg Pro Gln Thr Asp	Lys Lys Arg Val Tyr Arg			
	125		130		135
Val Leu Gln Cys	Arg Glu Gln Glu Leu	Thr Gln Met Ile Ser Thr			
	140		145		150
Leu Ser Asp Gly	Trp Arg Phe Glu Gln	Leu Ile Ser Met Gln Tyr			
	155		160		165
Thr Asn Tyr Gly	Pro Phe Glu Asn Asn	Glu Phe Leu Cys Val Val			
	170		175		180
Ser Lys Glu Cys	Gly Thr Thr Ala Gly	Arg Glu Leu Glu Leu Asn			
	185		190		195
Asp Arg Ala Lys	Val Leu Gln Gln Lys	Gly Ser Arg Ile Asn Thr			
	200		205		210
Ile Ser His Ser	Ala Thr Pro Thr Gln	His Gln Leu Asp Ala Ala			
	215		220		225
Lys Glu Ala Arg	Ala Thr Ala Thr Ala	Thr Ser Asn Thr Thr Asn			
	230		235		240
His Thr Arg Ser	Asp Gln Thr Gln Pro	Gln Ala Gln Ile Thr His			
	245		250		255
Gln Asp Gln Pro	Glu Ser Pro Lys Gln	Ser Pro Gln Gly Asp Tyr			
	260		265		270
Ala Ser Phe Ala	Phe Glu Thr Lys Leu	Thr Gly Thr Thr Ala Ile			
	275		280		285
Arg Phe Ser Pro	Leu Trp Pro Phe Cys	Ala Leu Tyr Glu Val Cys			
	290		295		300
Ala Gly Val His	Val Phe Asn Leu				
	305				

<210> 45

<211> 295

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> GenBank ID No: g2887407

<400> 45

Met Gln Pro Glu Gly Ala Glu Lys Gly Lys Ser Phe Lys Gln Arg		
1	5	10
Leu Val Leu Lys Ser Ser Leu Ala Lys Glu Thr Leu Ser Glu Phe		
	20	25
Leu Gly Thr Phe Ile Leu Ile Val Leu Gly Cys Gly Cys Val Ala		
	35	40
Gln Ala Ile Leu Ser Arg Gly Arg Phe Gly Gly Val Ile Thr Ile		
	50	55
Asn Val Gly Phe Ser Met Ala Val Ala Met Ala Ile Tyr Val Ala		
	65	70
Gly Gly Val Ser Gly Gly His Ile Asn Pro Ala Val Ser Leu Ala		
	80	85
Met Cys Leu Phe Gly Arg Met Lys Trp Phe Lys Leu Pro Phe Tyr		
		90

	95		100		105
Val Gly Ala Gln Phe Leu Gly Ala Phe		Val Gly Ala Ala Thr		Val	
	110		115		120
Phe Gly Ile Tyr Tyr Asp Gly Leu Met		Ser Phe Ala Gly Gly		Lys	
	125		130		135
Leu Leu Ile Val Gly Glu Asn Ala Thr		Ala His Ile Phe Ala		Thr	
	140		145		150
Tyr Pro Ala Pro Tyr Leu Ser Leu Ala		Asn Ala Phe Ala Asp		Gln	
	155		160		165
Val Val Ala Thr Met Ile Leu Leu Ile		Ile Val Phe Ala Ile		Phe	
	170		175		180
Asp Ser Arg Asn Leu Gly Ala Pro Arg		Gly Leu Glu Pro Ile		Ala	
	185		190		195
Ile Gly Leu Leu Ile Ile Val Ile Ala		Ser Ser Leu Gly Leu		Asn	
	200		205		210
Ser Gly Cys Ala Met Asn Pro Ala Arg		Asp Leu Ser Pro Arg		Leu	
	215		220		225
Phe Thr Ala Leu Ala Gly Trp Gly Phe		Glu Val Phe Arg Ala		Gly	
	230		235		240
Asn Asn Phe Trp Trp Ile Pro Val Val		Gly Pro Leu Val Gly		Ala	
	245		250		255
Val Ile Gly Gly Leu Ile Tyr Val Leu		Val Ile Glu Ile His		His	
	260		265		270
Pro Glu Pro Asp Ser Val Phe Lys Ala		Glu Gln Ser Glu Asp		Lys	
	275		280		285
Pro Glu Lys Tyr Glu Leu Ser Val Ile		Met			
	290		295		